



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 141074

TO: Andrew D Kosar
Location: REM/3C04/3C18
Art Unit: 1654
Monday, January 03, 2005

Case Serial Number: 10/800179

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes

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STIC-Biotech/ChemLib*141074*

From: Kosar, Andrew
Sent: Wednesday, December 22, 2004 3:47 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/800,179

Please search SEQ ID NO:19 in Application 10/800,179.

The claim is drawn to proteins 'comprising' SEQ ID NO:19.

Thank you,
Andrew Kosar

*Andrew D. Kosar, Ph.D.
Art Unit 1654
Office REMSEN 3Co4
Mail REMSEN 3C18
(571)272-0913*

RECEIVED
DEC 22 2005
STIC/CHL/BIOTEC
(STIC)

12/22/04

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[illegible][illegible]

XX
DR WPI; 1998-387091/33.
PT New recombinant protein polymers - containing naturally occurring
PT repetitive units for crosslinking by enzymes, useful as medical adhesives
PT and sealants, depots and matrices.
XX
PS Example 7; Col 43; 70pp; English.
XX
CC SELP8K polymer is a synthetic silk-like protein comprising multiple
CC copies of a monomer (see AAW9726) consisting of repeating units of silk-
CC like sequences (GAGAS) and elastin-like sequences (VPGVG) including a
CC reactive lysine residue. It was expressed in *Escherichia coli* from
CC plasmid pPT0345 as a 80 kDa protein. The SELP8K polymer was specifically
CC designed to be functionalised with different reagents reactive to amines.
CC Claimed recombinant protein polymers are capable of covalent crosslinking
CC by enzymatic reaction to form products which set quickly and have good
CC adhesive properties and high strength. The proteins can comprise a
CC repetitive amino acid backbone of repetitive units having collagen,
CC fibronin, elastin or keratin motifs and at least 2 enzyme recognition
CC sequences comprising a glutamine or lysine capable of enzyme catalysed
CC isopeptide formation. The products can be used as medical adhesives and
CC sealants, in the closure of wounds and repair of damaged tissue. (Updated
CC on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 884 AA;

Query Match 82.6%; Score 3448; DB 2; Length 884;
Best Local Similarity 90.6%; Pred. No. 5.7e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGASGVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGASGAGA 58
DB 34 GAGSGAGASGVGVPGVGVPGVGVPGKGVPGVGVPGVGVPGVGVPGAGASGAGA 93
QY 59 GSGAGASGAGASGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAS 114
DB 94 GSGAGASGAGASGVGVPGVGVPGKGVPGVGVPGVGVPGVGVPGAGAS 153
QY 115 GAGAGSGAGASGAGASGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGA 170
DB 154 GAGAGSGAGASGAGASGVGVPGVGVPGKGVPGVGVPGVGVPGVGVPGAG 213
QY 171 GAGSGAGASGAGASGAGASGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG 227
DB 214 GAGSGAGASGAGASGAGASGVGVPGVGVPGKGVPGVGVPGVGVPGAG 273
QY 228 -PGAGASGAGASGAGASGAGASGVGVPGVGVPGKGVPGVG-PGVG-PGVG- 283
DB 274 VPGAGAGSGAGASGAGASGAGASGVGVPGVGVPGVGVPGKGVPGVGVPGV 333
QY 284 PGVG-PGAGASGAGASGAGASGAGASGVGVPGVGVPGKGVPGVG-PGVG-P 340
DB 334 PGVGVPGAGAGAGAGASGAGASGAGASGVGVPGVGVPGVGVPGKGVPGV 393
QY 341 GVG-PGVG-PGAGAGAGAGAGAGAGASGAGASGVGVPGVGVPGKGVPGVG-PG 397
DB 394 GVGVPGVGVPGAGAGAGAGAGAGAGASGAGASGVGVPGVGVPGVGVPGKGV 453
QY 398 VG-PGVG-PGVG-PGAGAGAGAGAGAGAGASGAGASGVGVPGVGVPGKGV 454
DB 454 VGVPGVGVPGVGVPGAGAGAGAGAGAGAGASGAGASGVGVPGVGVPGVGV 513
QY 455 G-PGVG-PGVG-PGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
DB 514 GVPGVGVPGVGVPGVGVPGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 573
QY 511 VGVGV-PGVG-PGVG-PGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566
DB 574 VPGKGVPGVGVPGVGVPGVGVPGAGAGAGAGAGAGAGAGAGAGAGAGAG 633
QY 567 PGKGVPGVG-PGVG-PGVG-PGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 622

DB 634 PGVGVPGKGVPGVGVPGVGVPGAGAGAGAGAGAGAGAGAGAGAGAGAG 693
QY 623 GVGVPKGVPGVG-PGVG-PGVG-PGAGAGAGAGAGAGAGAGAGAGAGAG 678
DB 694 GVGVPGVGVPGKGVPGVGVPGVGVPGVGVPGAGAGAGAGAGAGAGAGAG 753
QY 679 VGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGAGAGAGAGAGAGAGAG 734
DB 754 VGVPGVGVPGVGVPGKGVPGVGVPGVGVPGAGAGAGAGAGAGAGAGAG 813
QY 735 GVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAGAGAGAGAG 780
DB 814 GVPGVGVPGVGVPGVGVPGKGVPGVGVPGVGVPGVGVPGAGAGAGAGAG 863

RESULT 6
AA51882
ID AAY51882 standard; protein; 884 AA.
XX
AC AAY51882;
XX
DT 22-JUN-2000 (first entry)
XX
DE Plasmid pPT0345 protein fragment containing SELP8K polymer units.

XX
KM Crosslinked protein; fibrin glue; tissue adhesive; sealant; SELP8K.
XX
OS Synthetic.
XX
PN US6033654-A.
PD 07-MAR-2000.
XX
PF 02-MAY-1996; 96US-00642246.
XX
PR 05-MAY-1995; 95US-00435641.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

PI Cappello J, Stedronsky ER;
XX
DR WPI; 2000-255682/22.
XX
PT Crosslinked protein composition, useful as tissue adhesive or sealant,
PT comprises peptide repeating units that contain functional groups reactive
PT with crosslinker.
XX
PS Example 2; Col 51-56; 45pp; English.

XX
CC This invention describes a novel crosslinked protein composition (A) in
CC which, before crosslinking, the protein (I) is new and comprises at least
CC 70 wt.% of repeating units GAGAS (1) and GVGVP (2), and in at least two
CC repeating units an amino acid (aa) is substituted by Lys or Arg to
CC provide a Lys/Arg equivalent weight of 1-20 kD. (I) contains at least two
CC aa having a functional group reactive with at least one of aldehyde,
CC iso(thio)cyanate and activated carboxy. (I) have similar biocompatibility
CC to fibrin glues, but set more quickly and give a bond with greater shear
CC strength. They are made from readily available natural sources, are easy
CC to administer and are gradually resorbed. This sequence represents a
CC crosslinking protein polymer unit designated SELP8K
XX
SQ Sequence 884 AA;

Query Match 82.6%; Score 3448; DB 3; Length 884;
Best Local Similarity 90.6%; Pred. No. 5.7e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGASGVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGASGAGA 58
DB 34 GAGSGAGASGVGVPGVGVPGVGVPGKGVPGVGVPGVGVPGVGVPGAGASGAGA 93
QY 59 GSGAGASGAGASGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGAGAS 114

[illegible]

RESULT 7	
ABG31412	
ID	ABG31412 standard; protein; 884 AA.
XX	
AC	ABG31412;
XX	
DT	29-NOV-2002 (first entry)
XX	
DE	SELP8K polymer encoded by plasmid pPT0345.
XX	
KW	protein polymer; functional group; crosslink; sealing; filling; tissue;
KW	tissue mass; tissue bonding; resorbable bond; flexible bond; sealant;
KW	adhesive; wound healing; burn dressing; blood flow; ruptured vessel;
KW	artery; vein; structural protein; vlnetary; fibroin; elastin; collagen
KW	keratin; SELP8K.
XX	
XX	Unidentified.
OS	Synthetic.
XX	
PN	US6423333-B1.
XX	
PD	23-JUL-2002.

XX 29-NOV-1999; 99US-00451206.
 XX
 PF 05-MAY-1995; 95US-00435641.
 XX
 PR 02-MAY-1996; 96US-00642246.
 XX
 XX
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 XX
 PI Stedronsky ER, Cappello J;
 XX
 DR WPI; 2002-672937/72.
 XX
 PT Crosslinked protein composition used as sealant or adhesive for sealing
 PT or filling defect in viable tissue, as burn dressing, or in wound healing
 XX e.g. to staunch flow of fluid e.g. blood, through ruptured vessels.
 XX
 PS Example 2; Col 17, 46pp; English.
 XX
 CC The present invention relates to protein polymers having repetitive units
 CC from naturally occurring structural proteins such as fibroin, elastin,
 CC collagen and keratin. The polymers comprise a functional group which can
 CC be chemically crosslinked with appropriate crosslinkers. The protein
 CC polymer is produced by recombinant DNA technology. The protein polymer is
 CC useful for sealing or filling a defect in viable tissue, particularly for
 CC augmenting tissue mass. The protein polymer is useful in a variety of
 CC applications related to their physical, chemical and biological
 CC properties, and/or to bond together separated tissue to provide a stable,
 CC flexible or resorbable bond. The protein is particularly useful as a
 CC sealant or adhesive, in wound healing or as a burn dressing e.g. to stop
 CC or staunch the flow of fluid (e.g. blood) through ruptured vessels (e.g.
 CC arteries or veins). The present sequence represents Selpak polymer
 SQ Sequence 884 AA;

Query Match	Similarity	82.6%	Score 3448	DB 517	Length 884
Best Local	Similarity	90.6%	Pred. No. 5.7e-217		
Matches	752	Conservative	0	Mismatches	26
				Indels	52
				Gaps	52
QY	3	GAGSGAGAGSGVGPVGVPBGKVPBGV-PGVG-PGVG-PGVG-PGAGAGSGAGA	58		
DB	34	GAGSGAGAGSGVGPVGVPBGKVPBGVGPVGVPBGVGPVGAGAGSGAGA	93		
QY	59	GSAGAGSGAGSGVGPVGVPBGKVPBGV-PGVG-PGVG-PGVG-PGAGAGS	114		
DB	94	GSAGAGSGAGSGVGPVGVPBGKVPBGVGPVGVPBGVGPVGAGAGS	153		
QY	115	GAGAGSAGAGSAGSGVGPVGVPBGKVPBGV-PGVG-PGVG-PGA	170		
DB	154	GAGAGSAGAGSAGSGVGPVGVPBGKVPBGVGPVGVPBGVGPBGV	213		
QY	171	GAGSGAGAGSGAGSGVGPVGVPBGKVPBGV-PGVG-PGVG-PGVG	227		
DB	214	GAGSGAGAGSGAGSGVGPVGVPBGKVPBGVGPVGVPBGVGPVG	273		
QY	228	- PGAGAGSGAGSGAGSGVGPVGVPBGKVPBGV-PGVG-PGVG-	283		
DB	274	VPAGAGSGAGSGAGSGVGPVGVPBGKVPBGVGPVGVPBGV	333		
QY	284	PGVG-PGAGSGAGSGAGSGVGPVGVPBGKVPBGV-PGVG-P	340		
DB	334	PGVGVPAGAGSGAGSGAGSGVGPVGVPBGVGPVGVPBGKVPBGV	393		
QY	341	GVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPBGKVPBGV-PG	397		
DB	394	GVGVPVGVPAGAGSGAGSGAGSGVGPVGVPBGVGPVGVPBGV	453		
QY	398	VG-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPBGKVPBGV	454		
DB	454	VGVPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPBGVGPVGVPBGK	513		
QY	455	G-PGVG-PGVG-PGAGAGSGAGSGAGSGVGPVGVPBGKVPBGV	510		
DB	514	GVGPVGVPVGVPAGAGSGAGSGAGSGVGPVGVPBGKVPBGV	573		

QY 511 VPGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSGVPGVPGVPGV 566
DB 574 VPGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 633
QY 567 PGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSGVPGVPGV 622
DB 634 PGVPGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 693
QY 623 GVGPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSGVPGV 678
DB 694 GVGPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 753
QY 679 VGVPGVPGVPGVPGV-PGVG-PGVG-PGVG-PGAGAGSAGAGSAGAGSGV 734
DB 754 VGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 813
QY 735 GVGPGVPGVPGVPGVPGV-PGVG-PGVG-PGVG-PGAGAGSAGAGS 780
DB 814 GVGPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 863

RESULT 8

ABM01628
ID ABM01628 strand; protein; 884 AA.

AC ABM01628;

DT 12-FEB-2004 (first entry)

DE Plasmid pPT0345 SELPak polymer protein.

KM Crosslinked protein; sealant; depot; drug; therapy; gel; film; thread;
coating; vlnlary.

OS Unidentified.

PN US2003104589-A1.

PD 05-JUN-2003.

PF 05-APR-2002; 2002US-00117931.

PR 05-MAY-1995; 95US-00435641.

PR 02-MAY-1996; 96US-00642246.

PR 29-NOV-1995; 99US-00451206.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

PI Stedronsky ER, Cappello J;

DR WPI; 2003-829350/77.

PT Crosslinked protein composition useful as sealing a defect in tissue, the
protein prior to crosslinking comprises repetitive units of 3-15 amino
acids of natural structural protein.

PS Example 2; Page 27-29; 0pp; English.

CC The present invention relates to crosslinked protein composition. The
invention is useful as sealants or depots to provide for relatively
uniform release of a physiologically active product e.g., drug and for
the formation of articles of manufacture such as gels, films, threads,
coatings. The present sequence is plasmid pPT0345 SELPak polymer protein
SQ Sequence 884 AA;

Query Match 82.6%; Score 3448; DB 7; Length 884;
Best Local Similarity 90.6%; Pred. No. 5.7e-217;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 58
|||||

DB 34 GAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 93

QY 59 GSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 114

DB 94 GSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 153

QY 115 GAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 170

DB 154 GAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 213

QY 171 GAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 227

DB 214 GAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 273

QY 228 -PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGV 283

DB 274 VPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGV 333

QY 284 PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGV 340

DB 334 PGVPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 393

QY 341 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 397

DB 394 GVGPGV 453

QY 398 VG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 454

DB 454 VGVPGV 513

QY 455 G-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 510

DB 514 GVGPGV 573

QY 511 VPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 566

DB 574 VPGKGVPGV 633

QY 567 PGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 622

DB 634 PGVPGKGVPGV 693

QY 623 GVGPGKGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 678

DB 694 GVGPGV 753

QY 679 VGVPGVPGVPGVPGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGV 734

DB 754 VGVPGV 813

QY 735 GVGPGVPGVPGVPGVPGVPGV-PGVG-PGVG-PGVG-PGAGAGSGAGAGS 780

DB 814 GVGPGV 863

RESULT 9

AAP82961
ID AAP82961 strand; protein; 2257 AA.

AC AAP82961;

DT 25-MAR-2003 (revised)

DT 27-NOV-1990 (first entry)

DE SEPL3 protein comprising gagage of silk fibroin and gvygp of elastin.

KM Repeat unit; collagen; keratin; immunisation; monomer; silk-like-protein;

KM SELP3; pSV1397; Bombyx mori; silk fibroin; elastin.

OS Synthetic.

FT Key Location/Qualifiers
Region 38..49

FT	/label= repeat_region
FT	/note= "gagags"
FT	38. .43
FT	/label= repeat_unit
FT	/note= "gagags found in natural elastin"
FT	50. .2260
FT	/label= repeat_region
FT	/note= "(gvgyvp)8 (gagags)8"
FT	50. .89
FT	/label= repeat_region
FT	/note= "vpvgv"
FT	50. .54
FT	/label= repeat_unit
FT	/note= "vpvgv found in silk fibroin protein"
FT	90. .117
FT	/label= repeat_region
FT	/note= "gagags"
FT	2161. .2201
FT	/label= repeat_region
FT	/note= "vpvgv"
FT	2202. .2231
FT	/label= repeat_region
FT	/note= "gagags"

FN	MO6605353-A.
XX	
PD	19-MAY-1988.
XX	
XX	
PF	29-OCT-1987; 87WO-US002822.
XX	
XX	
PR	04-NOV-1986; 86US-00927258.
XX	
PA	(SYTR) SYNTRO CORP.
XX	
PI	Ferrari FA, Richardson C, Chambers J, Causey SC, Pollock TJ;
XX	
DR	WPI; 1988-147587/21.
XX	
PT	DNA encoding oligopeptide repeating unit - used for producing silk-like
PT	protein, collagen, keratin or peptide(s) for immunisation.
XX	
PS	Disclosure; Page ?; 5pp; English

CC The SERP sequence present in PSY1377 encodes a protein of MM168,535. The
CC repeating unit gagaga is found in naturally occurring silk fibroin
CC protein. SILK-like proteins mimic the composition and physical properties
CC of silk of Bombyx mori. The repeating unit gagvg is found in naturally
CC occurring elastin The protein mimics the properties of elastin and
CC provides for elastomeric properties. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 2257 AA;

Query Match	79.0%;	Score 3296;	DB 1;	Length 2257;
Best Local Similarity	67.4%;	Pred. No. 8.8e-207;		
Matches 755; Conservative	0;	Mismatches 25;	Indels 340;	Gaps 52;

QY 1 GAGAGSGAGAGSGVGPVGVPVGVPVGKVPVG- PGVG- PGVG- PGV----- 46

Db 38 GAGAGSGAGAGSGVGPVGVPVGVPVGVPVGVPVGVPVGVPVGVPGAGAGSGA 97

QY 47 -----GPGAGAGSGAGAGSGAGAGSGAGAGSGVGPVGVP PGGKVP 92

0y 93 GVG-PGVG-PGVG-PGV-----GPGAGAGSGAGAGSGAGA 122

Db 158 GVGVPGVPGVPGVPGAGAGSAGSAGSAGSAGSAGSAGSAGA 211

Db 218 GSGAGGSSGVPGVGPVGVPGVGPVGVPGVGPAGAGSAGAGS 272
123 GSSAGAGSSGVPGVGPVGVPGVGPVGVPGVGPAGAGSAGAGS 18

0
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C
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F
G
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I
J
K
L
M
N
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[illegible]

[illegible]

ID	ADE44977	standard; protein; 2257 AA.
AC	ADE44977;	
DT	29-JAN-2004	(first entry)
XX		
DS	Recombinant structural protein SELP3 protein seq id 82.	
XX		
KW	recombinant protein; structural component; prosthetic device; synthetic fiber; structural protein; repeating oligopeptide; SELP3. Synthetic.	
OS		
PN	US2003083464-A1.	
XX		
PD	01-MAY-2003.	
PF	12-MAR-2002; 2002US-00096986.	
PR	04-NOV-1986; 86US-00927258.	
PR	29-OCT-1987; 87US-00114618.	
PR	22-APR-1993; 93US-00053049.	
PR	29-DEC-1993; 93US-00175155.	
PR	07-JUN-1995; 95US-00482085.	
PR	22-NOV-1999; 99US-00444791.	
PA	(PROT-) PROTEIN POLYMER TECHNOLOGIES INC.	
PI	Ferrari FA, Richardson C, Chambers J, Causey S, Pollock TJ,	
PI	Cappello J, Criseman JW;	
XX		
DR	WPI; 2003-810795/76.	
PT	New proteins useful as structural components of e.g. prosthetic devices and synthetic fibers, comprise at least one naturally occurring repeating unit of a naturally occurring structural protein.	
PS	Example 5; SEQ ID NO 82; 107pp; English.	
CC	The invention describes a novel recombinant protein (I) of at least 30 kDa comprising at least 50 percent of amino acids of at least one naturally occurring repeating unit of a naturally occurring structural protein, where a repeating unit comprises 3-20 amino acids, and where each of the same repeating unit comprises the same amino acids. (I) has a variety of uses including use as structural component of e.g. prosthetic devices and synthetic fibers. The protein has the properties of a naturally occurring structural protein but can be modified to have new properties. This sequence represents SELP3, a recombinant structural protein of the invention.	
CC		
CC		
CC		
XX		
Seq	Sequence 2257 AA:	
QY	Query Match	79.0%; Score 3296; DB ?; Length 2257;
Bt	Best Local Similarity	67.4%; Pred. No. 8,8e-207;
Mtches	Matches 755; Conservative 0; Mismatches 25; Indels 340; Gaps 52;	
Dd		
1	GAGAGSGAAGSvGVPGVGVPgGKGPVG-G-PGVG--PGVG-PGV-----	46
38	GAGAGSGAAGSvGVPGVGVPgGKGPVG-G-PGVG--PGVG-PGV-----	97
47	-----GPGAGAGSGAGSvGVPGVGVPgGKGPVG-G-PGVG--PGVG-PGV-----	92
Dd		
98	GAGSGAGAGSGAGSvGVPGVGVPgGKGPVG-G-PGVG--PGVG-PGV-----	157
QY	93 GYG-PGVG-PGVG-PGV-----GPGAGAGSGAGSGAGA	124
Dd	158 GVGVPGVGVPGVGVPgGKGPVG-G-PGVG--PGVG-PGV-----	217
QY	125 GSAGAGSGvGVPGVGVPgGKGPVG-V-PGVG-PGV-----	166

Biochemistry 23, 9677-9683, 1990

A:Title: Heterogeneity of rat tropoelastin mRNA revealed by cDNA cloning.

A:Reference number: A56106; MUID:91104868; PMID:1702999

A:Accession: A56106

A:Molecule type: mRNA

A:Residues: 1-864 <PTR>

A:Cross-references: UNIPROT:Q99372; GB:M60647; GB:J05292; NID:g207444; PIDN:AAA42269.1;

R:Deak, S.B.; Pierce, R.A.; Belsky, S.A.; Riley, D.J.; Boyd, C.D.

J. Biol. Chem. 263, 13504-13507, 1988

A:Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA.

A:Reference number: A30878; MUID:88330868; PMID:2971041

A:Accession: A30878

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 781-864 <DEA>

A:Cross-references: GB:J04035; NID:g207442; PIDN:AAA42268.1; PID:g207443

R:Frantzlan, C.; Pratt, C.A.; Farie, B.; Colaninno, N.M.; Offner, G.D.; Mogayzel Jr., P

J. Biol. Chem. 264, 15115-15119, 1989

A:Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle cells

A:Reference number: A56523; MUID:89359327; PMID:2768256

A:Accession: A56523

A:Molecule type: protein

A:Residues: 22-31 <FRA>

R:Rich, C.B.; Foster, J.A.

Arch. Biochem. Biophys. 268, 551-558, 1989

A:Title: Characterization of rat heart tropoelastin.

A:Reference number: 802173; MUID:89117149; PMID:2913947

A:Accession: 802173

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1P,369-545,548-764,770-864 <RIC>

A:Experimental source: heart

R:Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.

Genomics 12, 651-658, 1992

A:Title: Elements of the rat tropoelastin gene associated with alternative splicing.

A:Reference number: 154172; MUID:92241859; PMID:1572637

A:Accession: 154172

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 264-533 <RES>

A:Cross-references: GB:M66372; NID:g207455; PIDN:AAA42271.1; PID:g554527

A:Accession: 168505

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 558-864 <RE2>

A:Cross-references: GB:M66376; NID:g207459; PIDN:AAA42272.1; PID:g207462

C:Genetics:

A:Introns: 277/1; 292/1; 308/1; 339/1; 359/1; 419/1; 437/1; 467/1; 484/1; 601/1; 621/1;

A>Note: The list of introns may be incomplete

C:Superfamily: elastin

C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine

F:1-21/Domin: signal sequence #status predicted <SIG>

F:22-864/Product: elastin #status predicted <MAT>

F:854-859/Dsulfide Bonds: #status predicted

Query Match 28.4%; Score 1185; DB 1; Length 864;

Best Local Similarity 43.8%; Pred. No.5.4e-64;

Matches 378; Conservative 47; Mismatches 299; Indels 140; Gaps 57;

QY 15 GVPGV---GVPGVGVPGKGVPG---VGPVGVPVPG-VGPGA-----GAG-----SGAG 57

DB 23 GVPAGVPGVPG-GVPG-GVPGVYYPAGIGGGLPGCGKPRPGAGLGAFCAG 80

QY 58 AGSGAGSGAGSGAGSGVPGVPGVPGV-----PGKVPVPGVPGVPGVPGV 106

DB 81 PGGAGGAGPGAGLSTASRPGVLPVGGAGAAAYKAAKAGAGIGIG-GVPGVGVG 139

QY 107 GPGA-GAGSGAGAGSGAGSGAGSGAGSGVGP---GVGPVGVPVPGKVPVPGV-GPGVPG-G 161

DB 140 VPGAIVGVGIVGAVGIGTIGTIGLSTGAVVPLGAGVGAAGKPKG-VPGVGLGVYPGG 198

QY 162 VGPVG---PGAAGSGAGSGAGAG--SGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 215

Db 199 VLPGTARFPFGVVLPEVPTGTGKAVPGGGGGAFCSTPGVGPFGGQPGVPLGPIPA 258

Qy 216 PGVPGVPGVGVG-----AGAGSGAGSGAGAGSG-----AGAGSGVGVPG 258

Db 259 PXLPGVGLPYTNTKGLPYGVAAGAGKAGVPTGTGSGAAVAAAKAAKYGAGGGVLTG 318

Qy 259 VGVPGVPGVPGKGVPGVPGVGVGVG--PGVPGAGSGAGAGSGAGAGSGAG--AGSG 313

Db 319 VG-----GGGTPG-GAGAIPGIGITGAGTPAAAAAAKAAKAGAAAGLVPGGG 370

Qy 314 VGVPGVPGVGVGVG--KGVGVG--PGV--PGV-GPGVPGAGAGSGAGSGAGSGAGSG 367

Db 371 VVPGAGTPEVGLPGVGLTGVGGTPEVGGTPEVGGTPEVGGTPEVGGTPEVGGTPEV 429

Qy 368 AGAGSGVGV-PGVGVPGVPGVPGKVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 426

Db 430 AAKAAKYGAGVGTITTYGAGAGFPGVGVGAGAGLGGASGAAAAAAKAAKYGAG---- 486

Qy 427 GAGAGSGVGVPGVGVGVG--GVPGKGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 483

Db 487 GAGTGLGL-VPG-AVPGALPGAIVG-ALPGAIVGALPGAIVG-PGTGVPAGTTPAAAA 542

Qy 484 AGSGAGAGSGVPGVGVGVG--GVPG--KGV-GVPG--VGPVPGVGV--PG--AG 531

Db 543 AAAAAAATAKAGGYGLG-PGVGVPGVGVGGTPEVGGTPEVGGTPEVGGTPEVGGTPEV 601

Qy 532 AGSGAGAGSGAGAGS-----GAGAGSGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 587

Db 602 AGTTPAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 650

Qy 588 PGAG-GSGAGAGSGAGAGSGA--GAGSGVGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 640

Db 651 AGAGVPGFPGAIVGAGVPGSLAASKAAKYGAGAGLGGP-----GLGPGAGLGGPAG 706

Qy 641 GVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 700

Db 707 GVPGVGAGGAPAAAAAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA 765

Qy 701 GVPGVGPGVPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 756

Db 766 GAG-GVTPAGVGLGVSPAAAAKAAKYGAGLGLGAGLGLGAGLGLGAGLGLGAGLGL 823

Qy 757 GVPGVGPGVPGV--PGAGAGSGAGAG 778

Db 824 GGGAG-GLGVGKPRKPYGGALGA 846

RESULT 4

BABO

elastin precursor, splice form a - bovine

N:Alternate names: tropoelastin

N:Contains: elastin precursor, splice form b; elastin precursor, splice form c

C:Species: Bos primigenius taurus (cattle)

C:Date: 08-Jun-1989 #sequence, revision 26-Jul-1996 #text change 09-Jul-2004

C:Accession: A131865; A26728; B26728; C26728; A23343; I45886

R:Yeh, H.; Anderson, N.; Omswein-Goldstein, N.; Bashir, M.M.; Rosenblum, J.C.; Abrams, Biochemistry 28, 2365-2370, 1989

A:Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative splicing

A:Reference number: A131865; MUID:89274159; PMID:2543440

A:Accession: A131865

A:Molecule type: DNA

A:Residues: 1-27 <YEH>

A:Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:g340504; PIDD:AAA30777

R:Rajaj, K.; Anwar, R.A. 1987

J: Biol. Chem. 262, 5755-5762, 1987

A:Title: Primary structures of bovine elastin a, b, and c deduced from the sequences of A:Reference number: A92640; MUID:87194772; PMID:3032943

A:Accession: A26728

A:Molecule type: mRNA

A:Residues: 1,'RS','4-11','E','13-636','V','638-747' <RAB>

A:Cross-references: GB:J02717; NID:g163019; PIDD:AAA30503.1; PID:g163020

A:Accession: B26728

A:Molecule type: mRNA

A:Residues: 1, 'AS', '4-11, 'E', '13-225, 240-636, 'V', '638-747 <RA>
A:Cross-references: GB:K03505; NID:g163025; PIDN:AAA30505.1; PID:g163026
A:Accession: C26728
A:Molecule type: mRNA
A:Residues: 1, 'S8', '4-11, 'E', '13-225, 260-636, 'V', '638-747 <RA>
A:Cross-references: GB:K03506; NID:g163027; PIDN:AAA30506.1; PID:g163028
R:Cicella, G.; May, M.; Ormeau-Goldstein, N.; Indik, Z.; Morrow, S.; Yeh, H.S.; Rosenbl
Biochemistry 24, 3075-3080, 1985
A>Title: Structure of the 3' portion of the bovine elastin gene.
A:Reference number: A22343; PMID:85280426; PMID:2992576
A:Accession: A22343
A:Molecule type: DNA
A:Residues: 613-747 <CIC>
A:Cross-references: GB:M20415
R:Rosenbloom, J.
Lab. Invest. 51, 605-623, 1984
A>Title: Biology of disease: Elastin: Relation of protein and gene structure to disease.
A:Reference number: I45885; PMID:85059254; PMID:6150137
A:Accession: I45886
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 678-683, 685-747 <ROS>
A:Cross-references: GB:X31898; NID:g163015; PIDN:AAA96417.1; PID:g163018
R:Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
Biochem. Biophys. Res. Commun. 186, 549-555, 1992
A>Title: The cysteine residues in the carboxy terminal domain of tropoelastin form an in
A:Reference number: A58621; PMID:92337651; PMID:1632791
A:Contents: annotation, disulfide bonds
C:Comment: The term tropoelastin refers to a soluble precursor form of the extracellular
the oxidase activity.
C:Genetics: 634/3, 653/3, 676/3, 689/3, 707/3, 716/3, 733/3
A:introns: 634/3, 653/3, 676/3, 689/3, 707/3, 716/3, 733/3
A>Note: the list of introns is incomplete
C:Superfamily: elastin
C:Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F:1-747/Product: elastin precursor; splice form a #status predicted <EPa>
F:1-225, 260-747/Product: elastin precursor; splice form c #status predicted <EPc>
F:1-225, 240-747/Product: elastin precursor; splice form b #status predicted <EPb>
P:1-26/Domains: signal sequence #status predicted <SIG>
F:127-747/Product: elastin #status predicted <MAT>
F:105, 109, 252, 271, 275, 324, 327, 400, 404, 407, 445, 448, 489, 493, 544, 548, 552, 606, 609, 645, 649, 68
F:737-742/Disulfide bonds: #status experimental

Query Match 27.6%; Score 1151; DB 1; Length 747;
Best Local Similarity 41.4%; Pred. No. 5e-67;
Matches 350; Conservative 46; Mismatches 249; Indels 200; Gaps 45;

DQ 5 GSGAGAGSGGVP -GVGVPGVGVPKGKVGPGVPGVPG-----YGRPVG-----PGA 50
 | | | | | : | | | | | : | | | | | : | | | | |
DB 27 GGVPGAVPG -GVPPGVFFFGAGLGLGVGGGPGVKPAKPVGVLGPBLAGBSALPGA 85
 | | | | | : | | | | | : | | | | | : | | | | |
DQ 51 GAGSGAGAGSG -AGAGSGAGAGSGGVPGVPGVPGPKGVPGVPGVPGVPGVPGVPG 109
 ||| | | | | : | | | | | : | | | | | : | | | | |
DB 86 FPGGFPGAGGMAAAAYKAAAKAGAAGLVGGIG-----GVGGLCVSTG-----AVPRQ 136
 ||| | | | | : | | | | | : | | | | | : | | | | |
DQ 110 AGAGSGAGAGSGAGAGSGAGAGSGGVPGVPGVPGPKGVPGV--PGVPGVPGV 166
 ||| | | | | : | | | | | : | | | | | : | | | | |
DB 137 LGAGVGAGVPRK-----YPGVGHPGV-YPGGVLPFGAGARPPGI--GVLPGV 180
 ||| | | | | : | | | | | : | | | | | : | | | | |
DQ 167 GRPAGAGSGAGAGSGAGAGSGAGAGSGGVPGVPGVPG--KGVPRGVPGVPGV-- 223
 ||| | | | | : | | | | | : | | | | | : | | | | |
DB 181 PTGAGVPRKQVAGAPFA-----GIPGVGFPGGOPLPLGYPLTKAPLTPAGYL 230
 ||| | | | | : | | | | | : | | | | | : | | | | |
DQ 224 -----PGVPAGAGSGAGAGSGAGAGSG-----AGAGSGVPGVPGV-PGVGPV 267
 ||| | | | | : | | | | | : | | | | | : | | | | |
DB 231 PYRTGKLPLYGFGPGCVAGSAGKAATPTGTGVPDPAAAAAAKAAKLAAGAGAVLPBGVIG 290
 ||| | | | | : | | | | | : | | | | | : | | | | |
DQ 268 GKGVPGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGGVPGVPGVPGVPGV 327
 ||| | | | | : | | | | | : | | | | | : | | | | |
DB 291 GPGLPG-----APGAIPLTIGIAGVARDPAAAAAAAAAAKAAKAFGAAGLPGVPGVPGV 345
 ||| | | | | : | | | | | : | | | | | : | | | | |
DQ 328 GKGVPGVPGV-PGVG-PGVG-PGVG-PGAAGAGAGAGSGAGAGSGAGAGSGGVPGVPGV 383
 ||| | | | | : | | | | | : | | | | | : | | | | |

Db GVGVPGVGVPGVGVPGVGVPGVGV-----PGVGVPGVGVPG 386

OY 384 VGVPG-----KGVPGVP---GVPGPVGVPVPGAGSGAGS 420
| | | | | : | | | | | : | | | | | : | | | | |
Db VGVPGALSPAAATAKAATAKAAPGARAVIGIPTFGLGCGPFGIDAAAAPA-- 442
OY 421 GAGASGAGAGSGGVPGVGVPGVGVPGKVPGVPGVGVPGV- -PGVG- -PGAAGSGAG 477
| | | | | : | | | | | : | | | | | : | | | | |
Db 443 -----AAKAAKTGGVGLAGVVP--GAPALPGL- -PGVGVPGVGI.PAAAAAXAA 492
OY 478 AGSGAGAGSGAGAGSGGVPGVGVPGVGVPGKVPGVPGVPGVPGVPGVPGAGAGS 537
| | | | | : | | | | | : | | | | | : | | | | |
Db 493 KAAQGTLPBGVGAAPGVG----VPGVG----VPGV--GVAAGTGLGPPGGV.GAGVPA 542
OY 538 AGSGAGAGSGAGAGSGGVPGVGVPGVGVPGKVPGVPGVPGV- -PGVPGV- --GPGAAG 593
| | | | | : | | | | | : | | | | | : | | | | |
Db 543 AKSAKAAKAAKAQFRAAAGLIP-AGVPLGLV- -GAGVPLGVAGAVPGLGVAGVDPGPAVPG 600
OY 594 SGAGAGSGAGAGSGAGSGGVPGVGVPGVGVPGKVPGVPGVPGVPGVPGVPGAGAG 653
| | | | | : | | | | | : | | | | | : | | | | |
Db 601 TLAAKAAAFPGPGVGLAGVDLG--GAGLP-GVAGVPG----- 638
OY 654 SGAGAGSGAGAGSGAGSGGVPGVGVPGV- -VPGKVPGVPGVPGVPGVPGAGA 712
| | | | | : | | | | | : | | | | | : | | | | |
Db 639 - -AAAAAATAAKAAHFGILG- -GVGGLGVGSLGAVPG- -AVGLG- -GVSPAATAADAK 688
OY 713 GSAGAGSGAGAGSGAGSGGVPGVGVPGVGVPGKVPGVPGVPGVPGVPGAGA 772
| | | | | : | | | | | : | | | | | : | | | | |
Db 689 FGAAAGLGVLAGAGPEPPIGGAG-----GLGVGKPKRPFAGLALGALFPG- -GACL 738
OY 773 GSGAG 777
| | | | | : | | | | | : | | | | | : | | | | |
Db 739 GKSCG 743

RESULT 5

S59623

tropoelastin - sheep

CISpecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C.Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C.Accession: S59623; A24758

R.Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, F.; Christiano, A.M.; Deak, S.B.; Bo-

Matrix Biol. 14, 635-641, 1994

A>Title: Extensive alternate exon usage at the 5' end of the sheep tropoelastin gene.

A.Reference number: S59623

A.Accession: S59623

A.Molecule type: mRNA

A>Status: preliminary; not compared with conceptual translation

A.Residues: 1-770 <MAU>

A.Cross-References: UNIPROT:P11547

R.Yoon, K.; Davidson, J.M.; Boyd, C.; May, M.; LuValle, P.; Ornstein-Goldstein, N.; Smitt-

Arch. Biochem. Biophys. 241, 684-691, 1985

A.Title: Analysis of the 3' region of the sheep elastin gene.

A.Reference number: A24758; PMID:85305763; PMID:3839997

A.Accession: A24758

A.Molecule type: mRNA

A.Residues: 655-669, 671-716, 732-770 <YOO>

CISuperfamily: elastin

C.Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxyllysine

F.760-765/Dsulfide bonds: #status predicted

Query Match 27.5%; Score 1146.5; DB 2; Length 770;
Best Local Similarity 42.5%; Pred. No. 9, 5e-62;
Matches 368; Conservative 41; Mismatches 239; Indels 217; Gaps 52;

OY 5 GSGAGAGSGVVP- -GVGVGVGVPGKVPGVGVG- - - - -GCVGPVGPAGAG- - - - -SSGA- - - - - 56
| | | | | : | | | | | : | | | | | : | | | | |
Db 27 GGVLGAIVPG- -GVPGGVFFPGAIGLVGLGVGVPARKGVGLVPGGLAEESGLIPA 85
| | | | | : | | | | | : | | | | | : | | | | |
OY 57 - - - - -GAGGAG- - - - -AGSGAGAGSGGVPGVGVPGVGVPGKVPGVGVPGVPG 101
| | | | | : | | | | | : | | | | | : | | | | |
Db 86 GAPPGGFPAAGGAGAAATTAATAAGAGGLGVGIG- - -GVGGLGVSTCAVYPQLCAG 143

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: December 30, 2004, 12:51:15 ; Search time 202 Seconds

(Without alignments)
2221.744 Million cell updates/sec

Title: US-10-800-179-19

Perfect score: 4173
Sequence: 1 GAGAGSGAGAGSGVGVGVG.....GVGPGVPGAGAGSGAGAGS 780

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2107.5	50.5	5263	1 FBOH_BOMMO	P05790 bombyx mori
2	1916.5	45.9	897	2 Q6Q254	Q6Q254 agelenopsis
3	1916.5	45.9	897	2 AAT08436	AAT08436 agelenopsis
4	1531	36.7	760	2 Q6PY84	Q6PY84 kukulcania
5	1531	36.7	760	2 AAT08433	AAT08433 kukulcania
6	1459.5	35.0	1002	2 Q9BIU8	Q9BIU8 argiope tri
7	1451.5	34.8	988	2 O17434	O17434 nephila cia
8	1397.5	33.5	1553	2 Q6PFR0	Q6PFR0 candida gla
9	1365	32.7	1884	2 Q9NHW2	Q9NHW2 nephila ina
10	1314	31.5	750	1 ELS_CHICK	P07916 gallus gall
11	1312.5	31.5	1713	2 Q9VTR6	Q9VTR6 drosophi
12	1302.5	31.2	912	2 Q9BIT2	Q9BIT2 plectrurus
13	1302.5	31.2	2249	2 Q9NHW4	Q9NHW4 nephila cia
14	1297.5	31.1	1953	2 Q9BIT7	Q9BIT7 nephila ina
15	1274	30.5	1729	2 Q9U617	Q9U617 drosophi
16	1230.5	29.5	907	2 Q4C359	Q4C359 nephila cia
17	1219.5	29.2	860	2 Q8C9L8	Q8C9L8 mus musculu
18	1218	29.2	860	1 ELS_MOUSE	P54320 mus musculu
19	1215	29.1	810	2 Q9E5Z9	Q9E5Z9 mus musculu
20	1185	28.4	864	1 ELS_RAT	Q99372 ratu
21	1159	27.8	1071	2 Q7Y048	Q7Y048 drosophi
22	1142	27.4	747	1 ELS_BOVIN	P04985 bos taurus
23	1137	27.2	672	1 PHX5_MOUSE	P08399 mus musculu
24	1136	27.2	871	2 Q4C358	Q4C358 nephila cia
25	1122.5	26.9	707	2 Q28098	Q28098 bos taurus
26	1120.5	26.9	679	2 Q28097	Q28097 bos taurus
27	1100	26.4	666	2 Q28096	Q28096 bos taurus
28	1100	26.4	1217	2 Q8VIY9	Q8VIY9 mycobacteri
29	1096	26.3	1901	1 PG54_MYCTU	053553 mycobacteri
30	1094.5	26.2	992	2 Q7TWB8	Q7TWB8 mycobacteri
31	1089.5	26.1	1079	2 Q6MMW7	Q6MMW7 mycobacteri

32	1089.5	26.1	1079	2 CAE55606	CAE55606 mycobacte
33	1089	26.1	650	2 Q28099	Q28099 bos taurus
34	1087	26.0	1938	2 Q7TWC0	Q7TWC0 mycobacteri
35	1086	26.0	1715	2 Q8VI20	Q8VI20 mycobacteri
36	1084	26.0	1489	2 Q6MMW6	Q6MMW6 mycobacteri
37	1084	26.0	1489	2 CAE55607	CAE55607 mycobacte
38	1077	25.8	1460	2 Q9GUB5	Q9GUB5 gallieria me
39	1077	25.8	1468	2 Q9GUB5	Q9GUB5 nephila me
40	1041	24.9	747	1 SP01_NEPCL	P19837 nephila cia
41	1034	24.8	1660	2 Q79FD4	Q79FD4 mycobacteri
42	1034	24.8	1660	2 CAE55496	CAE55496 mycobacte
43	1034	24.8	1665	2 Q7D721	Q7D721 mycobacteri
44	1023.5	24.5	757	2 Q75MU5	Q75MU5 homo sapien
45	1023.5	24.5	757	2 AAS07435	AAS07435 homo bapi

ALIGNMENTS

RESULT 1
FBOH_BOMMO STANDARD; PRT; 5263 AA.
AC P05790; Q17220; Q26379;
DT 01-NOV-1988 (Rel. 09, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-UTL-2004 (Rel. 44, Last annotation update)
DE Fibroin heavy chain precursor (Fib-H) (H-fibroin).
GN Name=FIBH;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dioryssa; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20330362; PubMed=10871375;
RA Zhou C.-Z., Confalonieri F., Medina N., Zivanovic Y., Esnault C.,
Yang T., Jacquet M., Janin J., Duguet M., Petasso R., Li Z.-G.;
RT "Fine organization of Bombyx mori fibroin heavy chain gene.";
RL Nucleic Acids Res. 28:2413-2419(2000).
RN [2]
RP SEQUENCE OF 1-168 FROM N.A.
RX MEDLINE=80045039; PubMed=498286;
RA Tsujimoto Y., Suzuki Y.;
RT "The DNA sequence of Bombyx mori fibroin gene including the 5'
flanking, mRNA coding, entire intervening and fibroin protein coding
regions.";
RL Cell 18:591-600(1979).
RN [3]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=79211211; PubMed=455439;
RA Tsujimoto Y., Suzuki Y.;
RT "Structural analysis of the fibroin gene at the 5' end and its
surrounding regions.";
RL Cell 16:425-436(1979).
RN [4]
RP PARTIAL SEQUENCE FROM N.A.
RX STRAIN=Kinsu X Showa;
RC MEDLINE=89094688; PubMed=3210244;
RA Mita K., Ichimura S., Zama M., James T.C.;
RT "Specific codon usage pattern and its implications on the secondary
structure of silk fibroin mRNA.";
RL J. Mol. Biol. 203:917-925(1988).
RN [5]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=94365842; PubMed=7916056;
RA Mita K., Ichimura S., James T.C.;
RT "Highly repetitive structure and its organization of the silk fibroin
gene.";
RL J. Mol. Evol. 38:583-592(1994).
RN [6]
RP SEQUENCE OF 5179-5263 FROM N.A., AND DISULFIDE BONDS.
RC STRAIN=U-139;

Oy		155	GVP- GVPGVPGVPCGAGSAGASGAGSAGASGAGSVGP-- -VGVPGVPGK 209
Dd		272	GGGPQGAQPR- GAFEPGGGAAPFGQDGAFFPPGAAAGPCGPGCGPGAGGYG-- PG- 328
Oy		210	GVGVP- GVGPGVPGVPCGAGSAGASGAGSAGASGAGAAGSG----- VGVPGV 255
Dd		329	GAGYRPGVPGCAGAGTYPCGACGTCTGCSSPGCAGTCAGGBGPVTVDVTVTVEGV 388
Oy		260	GVPGVPGPKGVPGVPGVPGVPGVPGVPGAGSAGASGAGASGA----- GAGSGV 318
Dd		389	G-GPGCAGFCGAFPGCGAFCGCGAFCGAGPCAFCGCGCGCGCPGCVPGCAGCYGP 447
Oy		317	PGVPGVPGVPGPKGVNVP---- -GVPGVPGVPCGAGASG-- AGASGAGSAGAG 371
Dd		448	GGAG-- GVGPAATG-- GFPGAGAGFPCCGAGCFPGAGGFPGAGCYCPGCGVPGCA 503
Oy		372	SGVPGVPGVPGVPGVPG----- -KVPGVPG- GVPGVPGVPGCAGAS 414
Dd		504	CGTGPGGVG- PGGSSGCGAGCBGPVTVDVDSVGAFCGCTCGAAGPG- GAFFGCGGAGF 566
Oy		415	GAGAGSAGAGSAGAGSAGSVPG-- -VGVPGVPGKGVPGVPG- GVGPGVPGVPGAG 471
Dd		562	GPGCAGFCGCGAAGCGPCGCGCGPGCAGAGYG-- PG- GAGCYCPGVPCCGAGCYCPGCA 619
Oy		472	AGSGAGASGASAGSAGASG----- -VGVPGVPGVPGKGVPGVPGVPGV 522
Dd		620	GGTGPQSGSPGAGPCGAGBGPVTVDDVTVTPGEGV- GGPGCAGPCGAFGCGAGF 678
Oy		523	GPVCGPGA----- -GAGSAGASGAGSAGASGSVPGVPGVPGVPGKGV 571
Dd		679	GPGAGCAGPCGPCGPCGPCGPCGVCPCGACGTCPCGAGFCPCGCGPCGAGPG 738
Oy		572	PGVPGVPGVPGVPGVPGAGSAGASGAGSAGASGAGSAGSVPGVPGVPGK-- 628
Dd		739	PCGAGFCGCGAGFCGCGAGCYCPG- CVPCCGAGCFPG- GVPCCSGPCGAGBGPVT 796
Oy		630	----- -GVPGVP- GVPRGVPGVPCGAGSAGASGAGSAGASGAGSAGSVGPG-- 678
Dd		797	VDPVSVGAPCGCGPCGAGPG- GAFFGPGGAGFCPCGGAFFGCGAAGCPGSGCGCGP 855
Oy		679	VGVPGVPGVPGVPGVPG- GVPGVPGVPGPCGAGSAGASGAGSAGAGSAGASGAGSG-- 733
Dd		856	CGAGCTG- PG- GAGCTGPGCTVPCGAGCTGTCGAGAGTFCGCGAGPCGAGBGPVT 913
Oy		734	---- -VGVPGVPGVPGKGVPGVPGVPGVPGVPGVPGAGAGSAGAG 779
Dd		914	DVDVTPGPGVG- GCPGCGAGPCGAGFCGCGAGFCGCGAGPCGAGPCGPGCG 963
RESULT 7			
ID	017434	PRELIMINARY;	PRT; 988 AA.
AC	017434;		
DT	01-JAN-1998 (TrEMBLrel. 05, Created)		
DT	01-JUN-1998 (TrEMBLrel. 05, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Minor ampullate silk protein MspI (Fragment).		
OS	Nephila clavipes (Orb spider).		
OC	Eukaryote; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;		
OC	Aranemorphae; Enelegynae; Araneoldea; Tetragnathidae; Nephila.		
OX	NCBI_TaxID=6915;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98200471; PubMed=9541398;		
RA	Colgin M.A., Lewis R.V.;		
RT	"Spider minor ampullate silk proteins contain new repetitive sequences		
RL	and highly conserved non-silk-like 'spacer regions'.";		
DR	Protein Sci. 7:667-672(1998).		
FT	EMBL; AF027735; AAC14589.1; --		
FT	NON TER 1		
SO	SEQUENCE 988 AA; 79082 MW; 461E03DF53F7085D CRC64;		

	Query Match	34.8%;	Score 1451.5;	DB 2;	Length 988;	
	Best Local Similarity	39.4%;	Pred. No. 1.8e-66;			
	Matches 372;	Conservative 46;	Mismatches 286;	Indels 239;	Gaps 31.	
Oy	1	GAGAGSGAGAGSGGvGVPGVGPVGvPBGKGVPGVGPVGvPPVGPvPGAAGSAGAGS	60			
Db	2	GAASGAGAAAAGAGAGAGAGTG-----QIGGAGAGAGAAAAAGAGAGAAGTGR	52			
Oy	61	GAGAGSG--AGAGSGVPVGPVPGVGPBGKVPVGPvPG-----	101			
Db	53	GAGAGSGAAAAGAGSGAGAGYG-----GAGYGAAGAGAGSSAGNAFAQSLSNLLS	103			
Oy	102	-----VGPvGPdA-----GAGSG-----	115			
Db	104	SGDFVQMISTTTSDHVAVSVAQNVSQGLDAMANNLLGAVSGYSTLGNAISDA	163			
Oy	116	-----AGAGSGAGAG	125			
Db	164	SAYAAALSAIGNVLANSGISSESTASSAASAASVTTLTSYEPAPVYAASASGGYG	223			
Oy	126	SGAGAGSGVGPVGPVGPvBKGVPVGPvGPvGPvGPvBPvPGAAGSAGAGSGAGAG	185			
Db	224	AGAGAVAAAAAGAGAGGYGRGAGAGYGQG--GYGAGAGAGAAAAAGAGAGAGGYGAGAGAG	282			
Oy	186	SGAGAGSGVGPVCVGPVGPvPKGVPGV-----PVGPVCVGPVCPAGAAGSAGAGSG	241			
Db	283	AGAAAAGAGAGAGAGYCGCGGYGAGG--GAGAAAAAAGAGAGAGGYGRGAGAGAGAAAGAG	341			
Oy	242	AGA-----GSAGAGSGVGPVGPVGPvBKGVPVGPvGPvGPvGPv-----	286			
Db	342	AGGTGGGGYTGAGAGAGAAAAAGAGSGAGAGYGRGA--GAGAGAAAAGAGAGAGTGGGCG	400			
Oy	287	-GPAGAGSGAGAGSGAGA-----GSAGAGSGGV-----PVGPVGPvGPvBKGVPvBGP	337			
Db	401	YCAGAGAGAAAAAGAGAGAGYGRGAGAGAGAGAGAGAAABAAGAGAGAGAGYGQG---GYG	456			
Oy	338	VGPVGPVGPvPGAAGAGSGAGAGSGAGAGSGAGAGSVGPVGPvGPvBKGVPvBGP	397			
Db	457	AGAGAGAAAAAAGAGAGAGAGYGRGAGAGAGAAAAAGAGAGGYG-----GQSGYGAGAG	509			
Oy	398	VGPVGPVGPvPGAAGAGSGAGAGSGAGAGSGAGAGSVGPVGPvGPvBKGVPvBGP	457			
Db	510	AAAAAGAGAGAGYGRGAGAGAGAGAGAGAGAGAGAGAGYG-----GQ-----	555			
Oy	458	VGPVGPVGPvPGAAGAGSGAGAGSGAGAGSGAGAGSVGPVGPvGPvBKGVPvBGP	517			
Db	556	--GYGAGAGAGAAAAAGAGAGAGAGYGRGAGAGAGAA--GAGAGGYG--GQ--GYGAG	607			
Oy	518	VGPVGPVGPvPGAAGAGSGAGAGSGAGAGAGAGSVGPVGPvGPvBKGVPvBGP	577			
Db	608	AGAGAGAAAAATATGAGAGYGRGAGAGAGAGAGAAAGAGATG-----GAGYCGCGGYGAGAG	660			
Oy	578	VGPVGPVGPvPGAAGAGSGAGAGSGAGAGAGAGAGSVGPVGPvGPvBKGVPvBGP	637			
Db	661	AGAAAAAGAGAG--GACTYGRGAGAGAGAGAGAGAGAGAGAGAGAGAGAGYG--GQGTGAGAG	716			
Oy	638	VGPVGPVGPvPGAAGAG-----SGAGAGSGAGAGAGAG-----GSGVGPVGPV	681			
Db	717	AGAAAAAGAGAGAGYSTRGABAGAGAGAGAGAGAGAGAGYCGCGGYGAGAGAGAGAAA	776			
Oy	682	PVGPVGPvPKVGPVGPvGPvGPvBPvPGAAGSGAG-----AGSGAGAGSGAGAGSVGP	736			
Db	777	AGAGSGAGAG--GYGRGAGAGAGAGAGAGAGAGAGAGAGAGYCGCGGYGAGAGAGAGAGR	834			
Oy	737	PVGPVGPvGPvPKVGPvGPvGPvBPvPGAAGSGAGAG	779			
Db	835	GGYg--RGAGAGGYGCG-----GYGAGAGAGAGAGAGAGAGAG	869			
RESULT 8						
ID	06FPRO	PRELIMINARY;	PRT; 1553 AA.			
AC	06FPRO;					

DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	Similarities with tr Q08294 Saccharomyces cerevisiae YOL155C.
GN	ORFNames=CAGJ051771g
OS	Candida glabrata (Yeast) (Torulopsis glabrata).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX	NCBI_TaxID=5478;
RN	[1]
RP	SEQUENCE FROM N.A.
RG	STRAIN=CB5138;
RG	GENOLEVURES;
RA	Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA	Lafontaine I., de Montigny J., Marcq C., Neuvéglise C., Talla E.,
RA	Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA	Batnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA	Boisarme A., Boyer J., Catillolo C., Confaridoleri F., de Daruvar A.,
RA	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Giropi A.,
RA	Hartrey F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
RA	Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA	Nicaud J.M., Nikoleki M., Oztes S., Ozler-Kalogeropoulos O.,
RA	Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA	Swemene D., Tekcia F., Wesolowski-Jouvel M., Westhof E., Wirth B.,
RA	Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA	Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
RA	Winkler P., Souciet J.L.;
RT	"Genome evolution in yeasts."
RL	Nature 430:35-44(2004).
RL	EMBL; CR380956; CAG60731.1; --
DR	SEQUENCE 1553 AA; 145623 MW; A17810AE221D7480 CRC64;

[illegible]

[illegible]

RESULT 9

ID	Q9NHM2	PRELIMINARY;	PRT; 1884 AA.
AC	Q9NHM2;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, last annotation update)		
DE	Flagelliform silk protein (Fragment).		
GN	Name:Flag;		
OS	Nephila laurata madagascariensis.		
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;		
OC	Araneomorphae; Entelegynae; Araneoidae; Tetragnathidae; Nephila.		
OX	NCBI_taxonomy=115969;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20156766; PubMed=10688794;		
RA	Hayashi C.Y., Lewis R.V.;		
RT	"Molecular architecture and evolution of a modular spider silk protein gene";		
RL	Science 287:1477-1479(2000).		
DR	EMBL; AF218623; AAF36091.1; .		
DR	GO: GO:0005737; C:cytosolasm; IEA.		
DR	GO: GO:0006817; P:phosphate transport; IEA.		
DR	InterPro: IPR006160; Collagen.		
FT	NON_TER	1884	1884
QO	SEQUENCE	1884 AA; 148738 MW; 27B6F45339FD20A5 CRC64;	

Query Match

Best Local Similarity 42.3%; Pred. No. 6.2e-62;
Matches 412; Conservative 16; Mismatches 334; Indels 212; Gaps 65;

[illegible][illegible]

RESULT 10

ELS_CHICK	STANDARD:	PRT:	750 AA.
ID_ ELS CHICK			

DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Elastin precursor (Tropoelastin) (Fragment).
GN Name=ELN;
NC gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=67242320; PubMed=3593675;
RA Bressan G.M., Argos P., Stanley K.K.;
RT Repeating structure of chick tropoelastin revealed by complementary
RT DNA cloning.";
RL Biochemistry 26:1497-1503(1987).
RN [2]

RP	SEQUENCE OF 85-750 FROM N.A. (ISOCORM 2).
RX	MEDLINE=88309083; PubMed=2841924;
RA	Baile V.J., Foster J.A.;
RT	"Multiple chick tropoelastin mRNAs.;"
RL	Biochem. Biophys. Res. Commun. 154:1054-1060(1988).
RN	[3]
RP	SEQUENCE OF 457-750 FROM N.A.
RC	TISUS=Aorta;
RX	MEDLINE=87297534; PubMed=3502711;
RA	Tokimatsu I., Tajima S., Nishikawa T., Tajima M., Fukasawa T.;
RT	"Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcription of the elastin gene in developing chick embryo.;"
RL	Arch. Biochem. Biophys. 256:455-461(1987).
CC	-1- FUNCTION: Major structural protein of tissues such as aorta and nuclear ligament, which must expand rapidly and recover completely.
CC	-1- SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
CC	-1- SUBCELLULAR LOCATION: Extracellular matrix of elastic fibers.
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Comment=Additional isoforms seem to exist;
CC	Name=1;
CC	Isoid=P07916-1; Sequence=Displayed;
CC	Name=2; Synonyms=Embryonic;
CC	Isoid=P07916-2; Sequence=VSP_004241, VSP_004242;
CC	-1- PTM: The crosslinks are made of deaminated lys.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M18633; AAA48761.1; -.
DR	EMBL; M21880; AAA49082.1; -.
DR	EMBL; M15889; AAA49108.1; -.
DR	PIR; A26601; A26601.
DR	InterPro; IPR008160; Collagen.
DR	InterPro; IPR003979; tropoelastin.
DR	Plan; PF01391; Collagen; 1.
DR	PRINTS; PR01500; TROPOLASTIN.
KW	Alternative splicing; Connective tissue; Repeat; signal;
KW	Structural protein.
FT	NON TER 1 1
FT	SIGNAL <1 24
FT	CHAIN 25 750 Elastin.
FT	DOMAIN 83 686 8 X tandem repeats.
FT	REPEAT 83 127 1.
FT	REPEAT 219 262 2.
FT	REPEAT 263 318 3.
FT	REPEAT 319 393 4.
FT	REPEAT 394 482 5.
FT	REPEAT 483 554 6.
FT	REPEAT 555 619 7.
FT	REPEAT 620 686 8.
FT	DISULFID 739 745 By similarity.
FT	MOD_RES 63 63 Alysine (potential).
FT	MOD_RES 66 66 Alysine (potential).
FT	MOD_RES 111 111 Alysine (potential).
FT	MOD_RES 115 115 Alysine (potential).
FT	MOD_RES 156 156 Alysine (potential).
FT	MOD_RES 159 159 Alysine (potential).
FT	MOD_RES 198 198 Alysine (potential).
FT	MOD_RES 200 200 Alysine (potential).
FT	MOD_RES 235 235 Alysine (potential).
FT	MOD_RES 252 252 Alysine (potential).
FT	MOD_RES 256 256 Alysine (potential).
FT	MOD_RES 297 297 Alysine (potential).
FT	MOD_RES 301 301 Alysine (potential).
FT	MOD_RES 354 354 Alysine (potential).

FT	MOD_RES	357	357	Aligne (potential).
FT	MOD_RES	427	427	Aligne (potential).
FT	MOD_RES	431	431	Aligne (potential).
FT	MOD_RES	513	513	Aligne (potential).
FT	MOD_RES	517	517	Aligne (potential).
FT	MOD_RES	520	520	Aligne (potential).
FT	MOD_RES	520	520	Aligne (potential).
FT	MOD_RES	566	566	Aligne (potential).
FT	MOD_RES	590	590	Aligne (potential).
FT	MOD_RES	593	593	Aligne (potential).
FT	MOD_RES	655	655	Aligne (potential).
FT	MOD_RES	658	658	Aligne (potential).
FT	MOD_RES	719	719	Aligne (potential).
FT	MOD_RES	722	722	Aligne (potential).
FT	MOD_RES	743	743	Aligne (potential).
FT	MOD_RES	748	748	Aligne (potential).
FT	MOD_RES	750	750	Aligne (potential).
FT	VARSP_LIC	212	212	G -> GLGFGFGQPGVPLGYPRIKAPLPG (in isoform 2).
FT	FT			/FTId=VSP_004241.
FT	VARSP_LIC	501	501	G -> GVGVEFGVPGP (in isoform 2).
FT	FT			/FTId=VSP_004242.
FT	CONFLICT	536	536	A -> G (in Ref. 3).
FT	CONFLICT	571	571	P -> A (in Ref. 3).
FT	CONFLICT	610	610	P -> A (in Ref. 3).
FT	CONFLICT	654	654	A -> R (in Ref. 3).
FT	CONFLICT	667	667	P -> R (in Ref. 3).
FT	SEQUENCE	750	AA; 63697 MW; E57ECB0C6EBE56F CRC64;	
Query Match				
Best Local Similarity 31.5%; Score 1314; DB 1; Length 750;				
Matches 398; Conservative 34; Mismatches 19; Indels 206; Gaps 64				
OY	16	VPGV-----	-GVPGVVPDGKGVPGVPGVPGVPGVPGAGSGAGSGA	62
DB	9	LPGVLLFTLPASQGGVPG-ALPGGVP-----	-GGCFPPGAGVG-----	GLGA 52
OY	63	GAGSGAGAGSGVPEV-GVPEVG----	-VPKGVPGVPGVPG--PGVG-PGVPGAGAGS	114
DB	53	GLAGGLAGGKPLKPVSGGLGLGLGLQIPGAGVGGLAGLGPAAFPGAASAALKR		112
OY	115	GAGSGAGAGSGAGAGSGVPGVPGVPGVPGVPGVPG-VPPEVPGVPGVPGAGAG		173
DB	113	AAKAGAGLGVGIGLGVG--GVGVPG----	-GLVPGVVPQPGVGAAGRPKVPKAGI-	165
OY	174	SGAGAGSGAGAGSGAGAGSGVPGVPGV-PGVPGPKGVPVPGVPGV-----		220
DB	166	-----PGAPPGGGVLPKGAGIRFPGVGLPVGPPT-GTGIKAKKGAGAGFAGIRPGVRLPF		218
OY	221	--GVPGVPGAGAGSG-AGAGSGAGAGSGAGAGSGVPGVPGV-PGVPGPKGVPQVGP		276
DB	219	VNGIGPG-GIGAGVTLGKAGYPTGTGVDAOAAAKAAKYGAGVLPAG----	-GIPVG--	272
OY	277	GVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGAGVPGVPGVPGVPGVPGVPG		335
DB	273	GVVPGV--GVVPGAGVGGPAAAAAAKAAKAGATGAGV-----	-LFGAG--GVVPGV	320
OY	336	PGVG--PGVPGVPG--PGAAGSGAGAGSGAGAGSGAGSGVPGVPGVPGVPGVPGK		391
DB	321	PGVGVPGVLPVPGVGI-PGV--AGVGTAPGAAAAAAKAAKXKAGAVPGVPGVGI--GGV		375
OY	392	PGVPGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGV-GVPGV-GVPGK		449
DB	376	PGV-PGV-PGV-PGV-----	-PVPVPGVPGVPGVPGV--	403
OY	450	GVVPGVPGVPGVPGVPGVPGAGAGAGAGAGSGAGAGSGAGAGSGAGVPGVPGVPGVPGK		509
DB	404	GVPGV-PGVVPGVPGV-GPAAAAAAKAA--KAAFPAGVPGVPGVPG--AVPGVPGV		457
OY	510	GVPGVPGVPGVPGVPGVPGAGAGSGAGAGSGAGAGSGAGAGSGVPGVPGVPGVPG		568
DB	458	GVPGVPGVPGVPGV-----	-PGVPGVPGVPGVPGVPG	486
OY	569	KGVPGVPGV-PGVPGVPGVPGAGAGAGAGS-GAGAGSGAGAGSGAGV--VPVG--V		621

[illegible]

RA	MEDLINE=22426065; PubMed=12537566;
RA	Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA	Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA	George R.A., Hoskins R.A., Lavery T., Muzy D.M., Nelson C.R.,
RA	Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA	Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA	Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT	"Finishing a whole-genome shotgun: release 3 of the Drosophila
RT	melanogaster euchromatic genome sequence."
RL	Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN	[3]
RP	SEQUENCE FROM N.A.
EX	MEDLINE=22426070; PubMed=12537573;
RA	Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA	Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA	Ashburner M., Celniker S.E.;
RT	"The transposable elements of the Drosophila melanogaster euchromatin:
RT	a genomics perspective."
RL	Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22426093; PubMed=12537572;
RA	Misera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA	Hradecky P., Huang Y., Kaminker U.S., Millburn G.H., Prochnik S.E.,
RA	Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu I., Betman B.P.,
RA	Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA	Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA	Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA	Lewis S.E.;
RT	"Annotation of the Drosophila melanogaster euchromatic genome: a
RT	systematic review."
RL	Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN	[5]
RP	SEQUENCE FROM N.A.
RG	FLYBASE;
RL	Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN	[6]
RP	SEQUENCE FROM N.A.
RG	FLYBASE;
RL	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR	EMBL, AE003543, AA049980.2; -.
DR	FLYBase; FBgn0028573; prc.
DR	GO; GO:0005578; C:extracellular matrix; IDA.
DR	GO; GO:0007507; P:heart development; IMP.
DR	InterPro; IPR009765; Pericardin rpt.
DR	Pfam; PF07054; Pericardin rpt.; 3d.
SO	SEQUENCE 1713 AA; 163500 MW; 06f343AC07E155D0 CRC64;
<hr/>	
Query Match	31.5%; Score 1312.5; DB 2; Length 1713;
Best Local Similarity	39.3%; Pred. No. 2,7e-59;
Matches 415; Conservative 49; Mismatches 306; Indels 287; Gaps 77;	
OY	1 GAGAGSGAGAGSGVGVPGVG-VPGVG-PGKGVPGVG--PVGPPGAG 53
Db	144 GYGQQLCVGAQAAGAGCGPYGPBGVGTGGPVGSPGIGSQGTGAGCPGVSQPGLG 203
OY	54 SGAAAGS-GAGAGSGAAGAGSGVGVPGVG--PGVGV--PGVG----- 99
Db	204 GQTGAGCPGPGTSGOPVVAQTGTGTGPGIQAOPGVGTGTGAQQPGISGGQTARQP 263
OY	100 ----PGVG--PGVG-PGAGAGSG----AGAGS-GAGAGSGAGAGSGVGVPGVG-PGVG 146
Db	264 YVVPGVGAQTGTGIGQPEYGAOPGLTGQTGAQGPGYSQPIIGGQTGAQGPGYGNPVGGA 323
OY	147 -PGKVTPVG--PGVGPVG---PGVGPAGAAGSAGAGS-GAGAGSGAGAGSGVGPVG 199
Db	324 QVTGQDPGYAQAPDVGTGTGAGCPGVSQPGISGQTGAAGPGVGTGPTGVAQTGAAGPGY 383
OY	200 GV-PGVGV-PGKVTPVG---PGVGPVGPVGVGAAGSAGAGSGA-----GAGSGAGA 250
Db	384 GAQPVGAQTGAAGPVGSGSPGIGGQTGAAG-QPYTGSQPIETGQTGARQPGYSQPEYGA 442
OY	251 GSGVGVGVGV-PGVG-PGKVTPVG---PGVGPVG---PGAGSAGAGAGSG 301

Db	443	QTGAQDPGVGAQPPGVGAQTGAQDPGVGSQPGTGGQTGAQDPGVGSQPPGVGAQTGAQ-PG	501
QY	302	AGAGSGAGSGSGVPGVG--VPGV-GVPGKGVPGVG--PGVGPVG--PGVPGAAGS	354
Db	502	YGAQGVGAQTGAQGPVGVSQPGTGGQTGAQDPGVGTGTPGVGAQTGTGTGPVGAPGVGT	561
QY	355	GAGAGS-GAGAGSGAGSGSVGVPGVG-VPGV-PGKGVPGV--PGVG-----PGV	402
Db	562	QTGAQDPGVGSQPGTGGQTGAQDPGVGTGTPGVGAQTGTGTGPVGAPGVGTGAQGPV	621
QY	403	G--PGVG--PGAGSGAGSGAGSGAGSGAGSGSVGPVG-VPGV-GVPGKVPVG--	455
Db	622	GSQPGVGTGTPGVGAQTGTGTGPVGAPGVGGQTGAQDPGVGTGTPGTGGQTGAQDPGVGS	680
QY	456	--PGVGPVG--PGVPGAAGSGAGSGAGSGAGSGAGSGSVGPVGVPV--GVPGK	509
Db	681	QPGTGGQTGGGQPGVGSQIGGQTGAQGPS-YGSPGVGAQMGAGQPGVGTGTPVIGGQTGA	739
QY	510	GVPGVG--PGVG-----PGVG-----PGVPGAAGS	534
Db	740	GQPGVGGQTVGGSGSPFLTPQPEIGTSGPIGKLGCGQSEAKPQVMAQPGTGGPSRYGS	799
QY	535	GAGAGSGAGAG-SGAGAGSGV-----GVPGVG-VPGV--VPG--	568
Db	800	QPGTGGQTGGGQPGVGSQGTGGGQPGVCGQATTISGLPGVGTGTPGTGATLAVPQGH	859
QY	569	-----KGVPGV-----PGVG-----PGVG-----	579
Db	860	YGVETTPGVGTGQTNQPPGVGGQPAIGGQTGAQDPGVYFIQPGTGGQTGTSGRQPGYT	919
QY	580	--PGV-----PGVPGAAGSGAGSGAGS-GAGAGSGAGSGAGSGVGPVG-VPGVPGK	629
Db	920	QPGTGGQTGAQDPGVGSQGTGGGQIGAGQPGVGSQPGTGGQTGAQDPVGAPPGV-----	975
QY	630	GVPGVG--PGVG-----PGVG--PGVG-----PGAAGSGAGSGAGSGAGAG	671
Db	976	GQPGVGNQPGVGGQRTGAQDPGVGSQPGTGGQTGAQDPGVGAQPPGVGQDLGAGNPGVGGQ	1035
QY	672	SGVGPVG-VPGV-----GVPGKV-VPGV--PGV-----PGV--PGA	710
Db	1036	TGAQDPGVGSQGTGGQTGAQDPGVGVTPGVGGQGTGAQTAAGKPGTGGQPGTGGSVY	1095
QY	711	GAGSGAGSGAGSGAGSGAGSGVGPVGVPVG-VPG-----KGVPGVPVGVPVG	763
Db	1096	GTGGQTGGGSGTGGQ-PGVGTGQRTGAQDPGVGSLGTGGQATGAQDPGVGPDSQPGT	1154
QY	764	-----PGVG-----PGAAGSGAGAG	779
Db	1155	GQTVGGHGGYSQPGTGAAPVYGTGPPGGGQGTGVGG	1191

RESULT	12			
Q9BIT2				
ID	Q9BIT2	PRELIMINARY;	PRT;	912 AA.
AC	Q9BIT2;			
DT	01-JUN-2001	(TRMBLrefl. 17, Created)		
DT	01-JUN-2001	(TRMBLrefl. 17, Last sequence update)		
DT	01-OCT-2002	(TRMBLrefl. 22, Last annotation update)		
DE	Fibroin 1 (Fragment)			
OS	Plectreurys tristis (Spider)			
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;			
OC	Araneomorphae; Haplogynae; Plectreuridae; Plectreurys.			
OX	NCBI_Taxid=33319;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=21179804; Pubmed=11283372;			
RA	Gatesy J., Hayashi C., Mocrink D., Woods J., Lewis R.;			
RT	"Extreme diversity, conservation, and convergence of spider silk			
RT	fibroin sequences."			
RL	Science 291:2603-2605(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			

RA	Gatesy J.E., Hayashi C.Y.;			
RL	Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.			
RM	EMBL: AF350281; AAK30610.1; --			
DR				
FT	NON_PTER	1		
SQ	SEQUENCE	912 AA; 74131 MW; 0A9FE14AA60D3EB5 CXC64;		
Query Match	31.2%	Score 1302.5;	DB 2;	Length 912;
Best Local Similarity	32.8%	Pred. No. 5.8e-59;		
Matches 334; Conservative	55;	Mismatches 215;	Indels 413;	Gaps 21;

[illegible]

[illegible]

ID	1630	PGAAAAAAAAAGC	1641
RESULT 15			
Q9617			
Q9617	PRELIMINARY;	PRT; 1729 AA.	
AC	Q9617		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAY-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Pericardine.		
GN	Name=prc;		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxId=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Oregon R.		
RX	MEDLINE=22065272; PubMed=12070098;		
RA	Charlier A., Zaffran S., Astier M., Semeriva M., Graecos D.;		
RT	"Pericardin, a Drosophila type IV collagen-like protein is involved in		
RT	the morphogenesis and maintenance of the heart epithelium during		
RT	dorsal ectoderm closure."		
RL	Development 129:3241-3253(2002).		
DR	EMBL; AF203342; AAF13280.1; -.		
DR	FLYBASE; FBmn0028573; prc.		
DR	GO; GO:0005578; C:extracellular matrix; IDA.		
DR	GO; GO:007307; P:heart development; IMP.		
DR	InterPro; IPR009765; Pericardin_xpf.		
DR	Pfam; PF07054; Pericardin_xpf; 33.		
SQ	SEQUENCE 1729 AA; 164661 MW; DA9B1B7FAB5CDEDB CRC64;		
Query Match	30.5%;	Score 1274;	DB 2; Length 1729;
Best Local Similarity	38.6%;	Pred. No. 2.4e-57;	
Matches 406;	Conservative 56;	Mismatches 313;	Indels 276; Gaps 79
QY	1	GAGAGSAGAGSGVGPVG--PGVGV-PGKGVPGV-----PGVG--PGVG 43	
DB	161	GYSGLGVGAADAGCPGCGVGAQCGAGQPGYSGQTIGGQTAGQPGYSGQGTG 220	
QY	44	-----PGVPGAGAGSGAGAGS-GAGAGSGAGSGSVGPVG-VPGV-GVPGKVP 93	
DB	221	GQTGAGCPGVGSGPGIGGQTGAGQPGYSGQPGIGGQTGAGCPGVGSGQGTGAGQPG 280	
QY	94	VG--PGVG-----PGVG--PGVG-----PGAGAGSGAGAGSGAGA---GS--GAGA 130	
DB	281	YGSQPGIGGQTGAGQPGYGTGPGIGGQTGAGQPGYSGQPGIGGQTGAGQPGYSGQPGIG 340	
QY	131	GSQGVGPVG--PGV-GVPGKGVPGV--PGVG-----PGVGPVGPG-AGA 172	
DB	341	QTGAGQPGYGTGPGIGGQTGAGQPGYGTGPGIGGQTGAGQPGYGTGPGIGGQTGAGQPGY 400	
QY	173	GSAGAGSGAGAGS-----GAGAGSGVGPVG--PGVGV-PGKGVPGV--PGVG-- 219	
DB	401	GSQPGIGGQTGAGQPGYGTGPGIGGQTGAGQPGYGTGPGIGAGQAGAGQPGYGTGPGIGG 460	
QY	220	-----PGVG--PGVG-----PGAGAGSGAGAGSGAGA---GS--GAGAGSGVGPVG 260	
DB	461	TGAGQPGYGTGPGIGTGTGAGQPGYSGQPGIGAGTGAQAGQPGYSGQPGIGGQTGAGQPGY 520	
QY	261	-VPGV-GVPGKGVPGV--PGVGPGV--PGVGPVG--PGVGPVGAGAGAGAGS-GAGAGSGAGAGS 312	
DB	521	SGQPGIGGQTGAGQPGYGTGPGIGAGTGAQAGQPGYSGQPGIGGQTGAGQPGYSGQPGIGGQT 580	
QY	313	GVGPGVGV--PGVG--PGKGVPGV--PGVGPVG--PGVGPVGAGAGAGAGS-GAGA 364	
DB	581	GAGQPGYGTGPGIGAGTGTGPGYSGQPGYSGQPGYGTGPGIGAGQPGYSGQPGIGGQTGAGQPGYSG 640	
QY	365	GSAGAGSGVGPVG--PGVGV-PGKGVPGV--PGVGPVG--PGVGPVG--PGAGAGSG 415	
DB	641	QPGIGGQTGAGQPGYGTGPGYSGQPGYSGQPGYGTGPGIGAGTGAQAGQPGYSGQPGIGGQTG 700	

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QY 416 AGAGSGAGAGSGAGAGSGVGPVGV--PGV-GVPGKVPGVG--PGVGPVG---PGVGP 468
Db 701 PGQ-PGYGTQPGVGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 759
QY 469 GAGAGSGAGAGSGAGAGSGAGAGSGVGPVGV--GVPGKVPGVG--PGV----- 519
Db 760 QIGGQTGAQGPS--YSGQPGVGAONGGGQGYGTTRPYIGGQTGAQGPYGGGQTVGSSPGF 818
QY 520 ---PGVG-----PGVGPAGAGSGAGAGSGAGAG--SGAGA 550
Db 819 LTQPGIGGIGISPIGKVGGGGQSEAAKPGYMAQPGIGSPRYGSQPGIDQTAGAGSGYCG 878
QY 551 GSGV-----GVPGV--PGV-----VPG-----KGVPGV----- 575
Db 879 QPGISGQTGGGQPGYGGQATISGLPGYGTQPGIGALTAVPGGHYGYETQPGIGGQTGTNQ 938
QY 576 PGVG--PGVG-----PGVG-----PGAGAGSG--AGAGSGAGAGSGAGAGSGVGPVGVG- 620
Db 939 PGFGGQPGIGGQTGAQGPYGVGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 998
QY 621 VPGV-GVPGKVPVGVG--PGVG-----PGVG-----PGAGAGSGAGAGSG 661
Db 999 QPGIGGQTGAQGPYGSQPGVGGQIGAGQPGYGSQPGIGGQTGAQGPYGAQPGFGGQPG 1058
QY 662 AGAGSGAGAGSGAGAGSGVGPVGV--VPGV-GVPGKVPVGPVGPVGV--PGVG-----PGA 710
Db 1059 YGNQPGVGGQTGAQGPYGSQPGVGGQTGAQGPY--GVTPGFGGQPGIGGQTAAAGKPGY 1116
QY 711 GAGSGAGAGSGAGAGSGAGAGSGV--GVPGVGV--PGVGPVPGK--VPGV-----P 756
Db 1117 GGGQPGIGSSPVYGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1176
QY 757 GVGPGVGPVG-----PGAGAGSGAGAG 779
Db 1177 GYGPSSQPGIGGAPVYGTQPGGGGQTVGIGG 1207

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Search completed: December 30, 2004, 12:54:58
 Job time : 215 sec8

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:51:21 ; Search time 23 Seconds

(without alignments)
2249.045 Million cell updates/sec

Title: US-10-800-179-19

Perfect score: 4173
Sequence: 1 GAGAGSGAGAGSGVGPVG.....GVGPVGPGAGAGAGAGS 780

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3526	84.5	889	3 US-08-806-029-19	Sequence 19, Appl
2	3448	82.6	884	1 US-08-397-633A-68	Sequence 68, Appl
3	3448	82.6	884	2 US-08-435-641-15	Sequence 15, Appl
4	3448	82.6	884	2 US-08-707-237A-96	Sequence 96, Appl
5	3448	82.6	884	3 US-08-642-246-15	Sequence 15, Appl
6	3448	82.6	884	4 US-09-451-206-15	Sequence 15, Appl
7	3448	82.6	884	5 PCT-US96-06229-15	Sequence 15, Appl
8	3296	79.0	2257	1 US-08-175-155-47	Sequence 47, Appl
9	3296	79.0	2257	1 US-08-477-509B-82	Sequence 82, Appl
10	3296	79.0	2257	2 US-08-707-237A-53	Sequence 53, Appl
11	3296	79.0	2257	3 US-08-482-085B-82	Sequence 82, Appl
12	3296	79.0	2257	3 US-09-444-791A-80	Sequence 80, Appl
13	3296	79.0	2257	3 US-08-397-633A-54	Sequence 54, Appl
14	3296	79.0	2257	3 US-08-175-155-47	Sequence 47, Appl
15	3296	79.0	2257	3 US-08-477-509B-82	Sequence 82, Appl
16	3296	79.0	2257	3 US-08-707-237A-53	Sequence 53, Appl
17	3296	79.0	2257	3 US-08-482-085B-82	Sequence 82, Appl
18	3296	79.0	2257	3 US-09-444-791A-80	Sequence 80, Appl
19	3296	79.0	2257	3 US-08-397-633A-54	Sequence 54, Appl
20	3296	79.0	2257	3 US-08-175-155-47	Sequence 47, Appl
21	3296	79.0	2257	3 US-08-477-509B-82	Sequence 82, Appl
22	3296	79.0	2257	3 US-08-707-237A-53	Sequence 53, Appl
23	3296	79.0	2257	3 US-08-482-085B-82	Sequence 82, Appl
24	3296	79.0	2257	3 US-09-444-791A-80	Sequence 80, Appl
25	3296	79.0	2257	3 US-08-397-633A-54	Sequence 54, Appl
26	3296	79.0	2257	3 US-08-175-155-47	Sequence 47, Appl
27	3296	79.0	2257	3 US-08-477-509B-82	Sequence 82, Appl

28	3158	75.7	2055	2 US-08-707-237A-52	Sequence 52, Appl
29	3158	75.7	2055	3 US-08-482-085B-81	Sequence 81, Appl
30	3158	75.7	2055	3 US-09-444-791A-81	Sequence 81, Appl
31	3089	74.0	2018	3 US-09-444-791A-80	Sequence 80, Appl
32	3089	74.0	2100	1 US-08-477-509B-80	Sequence 80, Appl
33	3089	74.0	2100	3 US-08-482-085B-80	Sequence 80, Appl
34	3089	74.0	2107	1 US-08-175-155-45	Sequence 45, Appl
35	3089	74.0	2107	2 US-08-707-237A-51	Sequence 51, Appl
36	2998	71.8	1056	1 US-08-212-237-6	Sequence 6, Appl
37	2998	71.8	1056	3 US-08-806-029-29	Sequence 29, Appl
38	2998	71.8	1056	5 PCT-US95-02772-6	Sequence 6, Appl
39	2855	68.4	1002	2 US-08-707-237A-103	Sequence 103, Appl
40	2855	68.4	1002	3 US-08-642-246-25	Sequence 25, Appl
41	2855	68.4	1002	4 US-09-451-206-25	Sequence 25, Appl
42	2855	68.4	1002	5 PCT-US96-06229-25	Sequence 25, Appl
43	2830	67.8	750	3 US-08-806-029-25	Sequence 25, Appl
44	2814	67.4	696	3 US-08-806-029-36	Sequence 36, Appl
45	2795	67.0	936	2 US-08-707-237A-108	Sequence 108, Appl

ALIGNMENTS

RESULT 1
US-08-806-029-19
Sequence 19, Application US/08806029
Patent No. 6380154
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
TITLE OF INVENTION: Delivery and Tissue Augmentation
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Flehr, Hombach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 889 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-806-029-19
Query Match 84.5%; Score 3526; DB 3; Length 889;
Best Local Similarity 92.2%; Pred. No. 3.3e-252;
Matches 765; Conservative 0; Mismatches 13; Indels 52; Gaps 52;
QY 3 GAGSAGAGSGVGPVGVPVGKVPVG-PGVG-PGVG-PGVG-PGAGSAGGA 58

[illegible]

RESULT 2
US-08-397-633A-68
; Sequence 68, Application US/08397633A
; Patent No. 5773577
; General Information:
; Applicant: Cappello, Joseph
; Title Of Invention: PRODUCTS COMPRISING SUBSTATESCAPABLE
; Title Of Invention: OF ENZYMAITIC CROSS-LINKING
; Number Of Sequences: 105
; Correspondence Address:
; Address: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; Street: 4 Embarcadero Center, Suite 3400
; City: San Francisco
; State: California
; Country: USA
; Zip: 94111-4187
; Computer Readable Form:

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1      MEDIUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: PatentIn Release #1.0, Version #1.25
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/08/397,633A
7      FILING DATE:
8      CLASSIFICATION: 530
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Rowland, Bertram I
11     REGISTRATION NUMBER: 20,015
12     REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: (415) 781-1989
15     TELEFAX: (415) 398-3249
16     TELEX: 910 277299
17     INFORMATION FOR SEQ. ID NO: 68:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 884 amino acids
20     TYPE: amino acid
21     STRANDEDNESS: single
22     TOPOLOGY: linear
23     MOLECULE TYPE: protein
24     US-08-397-633A-68

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[illegible]

TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2257 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-175-155-47

Query Match 79.0%; Score 3296; DB 1; Length 2257;
 Best Local Similarity 67.4%; Pred. No. 5, 8e-235;
 Matches 755; Conservative 0; Mismatches 25; Indels 340; Gaps 52;

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DB 38 GAGAGSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 97
QY 47 -----GPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 92
DB 98 GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 157
QY 93 GVG-PGVG-PGVG-PGV-----GPGAGAGSGAGAGSGAGAG 124
DB 158 GVGPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 217
QY 125 GSGAGAGSGVPGVPGVPGVPGKGVPGV-G-PGVG-PGVG-PGV----- 166
DB 218 GSGAGAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 277
QY 167 -----GPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 215
DB 278 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 337
QY 216 PGVG-PGVG-PGV-----GPGAGAGSGAGAGSGAGAGSGA 248
DB 338 PGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 397
QY 249 GAGSGVPGVPGVPGVPGKGVPGV-G-PGVG-PGVG-PGV----- 286
DB 398 GAGSGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 457
QY 287 -----GPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 339
DB 458 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 517
QY 340 -PGVG-PGV-----GPGAGAGSGAGAGSGAGAGSGAGAGS 372
DB 518 VPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 577
QY 373 GVGPGVPGVPGVPGKGVPGV-G-PVG-PGVG-PGV----- 406
DB 578 GVGPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 637
QY 407 --GPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 462
DB 638 GAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 697
QY 463 G-PGV-----GPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 496
DB 698 GVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 757
QY 497 PGVPGVPGVPGVPGKGVPGV-G-PVG-PGVG-PGV-----GP 528
DB 758 PGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 817
QY 529 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 585
DB 818 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 877
QY 586 Y-----GPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 620

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DB 878 VGPVPGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 937
QY 621 VPGVPGKGVPGV-G-PVG-PGVG-PGV-----GPGAGA 652
DB 938 VPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 997
QY 653 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 706
DB 998 GSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1057
QY 707 -----GPGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 744
DB 1058 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSG 1117
QY 745 GVPKGVPGV-G-PVG-PGVG-PGV-G-PVAGAGSGAGAGS 780
DB 1118 GVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 1157

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RESULT 9

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US-08-477-509B-82
; Sequence 82, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A
; APPLICANT: Cappello, Joseph
; APPLICANT: Cristman, John W
; APPLICANT: Dorman, Mary A
; TITLE OF INVENTION: No. 5770697e1 Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,509B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-398-3249
; TELEFAX: 415-781-1989
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2257 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-806-029-27

Query Match 78.0%; Score 3253; DB 3; Length 832;
Best Local Similarity 88.9%; Pred. No. 3.6e-232;
Matches 742; Conservative 0; Mismatches 13; Indels 80; Gaps 65;

QY 9 GAGSGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGSGAGAG 65
DB 3 G-----VGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 57
QY 66 SGAGAGS--GVGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGS 120
DB 58 SGAGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 116
QY 121 GAGAGSGAGAGS--GVGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSG 175
DB 117 GAGAGSGAGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 175
QY 176 AGAGSGAGAGSGAGAGS--GVGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVGPGA 230
DB 176 AGAGSGAGAGSGAGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGV 234
QY 231 GAGSGAGAGSGAGAGSGAGAGS--GVGVPGVPGVPGKGVPGVG-PGVG-PGVG-PG 285
DB 235 GAGSGAGAGSGAGAGSGAGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 294
QY 286 VGPAGAGSGAGAGSGAGAGSGAGAGS--GVGVPGVPGVPGKGVPGVG-PGVG-PG 341
DB 295 VG-GAGAGSGAGAGSGAGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 353
QY 342 VG-PGVPGAGAGSGAGAGSGAGAGS--GVGVPGVPGVPGKGVPGVG-PG 397
DB 354 VGVPGVG-GAGAGSGAGAGSGAGAGSVPGVPGVPGVPGVPGVPGVPGVPGVPG 412
QY 398 VG-PGVG-PGVGPGAGAGSGAGAGSGAGAGS--GVGVPGVPGVPGKGVPG 453
DB 413 VGVPGVPGVPGV-GAGAGSGAGAGSGAGAGSVPGVPGVPGVPGVPGVPGVPG 471
QY 454 VG-PGVG-PGVGPGAGAGSGAGAGSGAGAGS--GVGVPGVPGVPGVPG 508
DB 472 VGVPGVPGVPGVPGV-GAGAGSGAGAGSGAGAGSVPGVPGVPGVPGVPG 530
QY 509 KGVPGVG-PGVG-PGVGPGAGAGSGAGAGSGAGAGS--GVGVPGVPGVPG 563
DB 531 VGVPGVPGVPGVPGVPGVPGV-GAGAGSGAGAGSGAGAGSVPGVPGVPGVPG 589
QY 564 VGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGSGAGAGS--GVGVPG 618
DB 590 VGVPGVPGVPGVPGVPGVPGVPGV-GAGAGSGAGAGSGAGAGSVPGVPGVPG 648

QY 619 VGVPGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGSGAGAGS--G 673
DB 649 VGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 707
QY 674 VGVPGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGSGAGA 730
DB 708 VGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 766
QY 731 GS--GVGVPGVPGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGS 780
DB 767 GSVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPGVPG 820

Search completed: December 30, 2004, 12:58:12
Job time : 33 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 12:51:21 ; Search time 148 Seconds
(without alignments)
1895.862 Million cell updates/sec

Title: US-10-800-179-19

Perfect score: 4173

Sequence: 1 GAGAGSGAGAGSGVGPVG.....GVGPVGAGAGSGAGAGS 780

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4173	100.0	780	15	US-10-441-965-19 Sequence 19, Appl
2	4173	100.0	780	16	US-10-800-179-19 Sequence 19, Appl
3	4173	100.0	780	17	US-10-845-936A-19 Sequence 19, Appl
4	4173	100.0	780	17	US-10-845-936A-19 Sequence 19, Appl
5	3526	84.5	889	8	US-08-806-029-19 Sequence 19, Appl
6	3448	82.6	884	14	US-10-117-931-15 Sequence 15, Appl
7	3448	82.6	884	16	US-10-800-179-25 Sequence 25, Appl
8	3448	82.6	884	17	US-10-845-936A-25 Sequence 25, Appl
9	3448	82.6	884	17	US-10-845-936A-25 Sequence 25, Appl
10	3448	82.6	983	17	US-10-845-936A-32 Sequence 32, Appl
11	3448	82.6	1027	17	US-10-845-936A-32 Sequence 32, Appl
12	3448	82.6	1105	17	US-10-845-936A-33 Sequence 33, Appl
13	3448	82.6	1125	17	US-10-845-936A-34 Sequence 34, Appl

14	3346	80.2	965	16	US-10-800-179-31	Sequence 31, Appl
15	3346	80.2	965	17	US-10-845-936A-31	Sequence 31, Appl
16	3346	80.2	965	17	US-10-845-936A-31	Sequence 31, Appl
17	3305	79.2	1038	16	US-10-800-179-30	Sequence 30, Appl
18	3305	79.2	1038	17	US-10-845-936A-30	Sequence 30, Appl
19	3305	79.2	1038	17	US-10-845-936A-30	Sequence 30, Appl
20	3296	79.0	1016	17	US-10-096-986-82	Sequence 82, Appl
21	3263	78.2	1016	17	US-10-845-936A-36	Sequence 36, Appl
22	3253	78.0	832	8	US-08-806-029-27	Sequence 27, Appl
23	3250	77.9	1043	17	US-10-845-936A-35	Sequence 35, Appl
24	3192	76.5	768	8	US-08-806-029-35	Sequence 35, Appl
25	3182	76.3	988	8	US-08-806-029-28	Sequence 28, Appl
26	3176	76.1	1465	14	US-10-096-986-74	Sequence 74, Appl
27	3158	75.7	2055	14	US-10-096-986-81	Sequence 81, Appl
28	3089	74.0	2018	14	US-10-096-986-80	Sequence 80, Appl
29	2998	71.8	1056	8	US-08-806-029-29	Sequence 29, Appl
30	2859.5	68.5	696	15	US-10-441-965-21	Sequence 21, Appl
31	2855	68.4	1002	14	US-10-117-931-25	Sequence 25, Appl
32	2830	67.8	750	8	US-08-806-029-25	Sequence 25, Appl
33	2814	67.4	696	8	US-08-806-029-36	Sequence 36, Appl
34	2810	67.3	696	15	US-10-441-965-23	Sequence 23, Appl
35	2795	67.0	936	14	US-10-117-931-30	Sequence 30, Appl
36	2740	65.7	966	14	US-10-117-931-34	Sequence 34, Appl
37	2676	64.1	953	8	US-08-806-029-14	Sequence 14, Appl
38	2655.5	63.9	1011	14	US-10-096-986-94	Sequence 94, Appl
39	2654	63.6	936	8	US-08-806-029-26	Sequence 26, Appl
40	2643	63.3	972	8	US-08-806-029-30	Sequence 30, Appl
41	2621	62.8	1024	8	US-08-806-029-31	Sequence 31, Appl
42	2463	59.0	1169	8	US-08-806-029-33	Sequence 33, Appl
43	2420	58.0	1040	8	US-08-806-029-32	Sequence 32, Appl
44	2281.5	54.7	1136	8	US-08-806-029-9	Sequence 9, Appl
45	2281.5	54.7	1177	14	US-10-096-986-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1
US-10-441-965-19
; Sequence 19, Application US/10441965
; Publication No. US20040014186A1
; GENERAL INFORMATION:
; APPLICANT: KIMAR, MANOI
; TITLE OF INVENTION: SYNTHESIS OF INORGANIC STRUCTURES USING TEMPLATON AND
; FILE REFERENCE: DOC 0061 PA
; CURRENT APPLICATION NUMBER: US/10/441,965
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/381,913
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polymer
US-10-441-965-19

Query Match 100.0%; Score 4173; DB 15; Length 780;
Best Local Similarity 100.0%; Pred. No. 8.9e-248;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGSGAGAGSGVGPVGVPVGKGVGPVGVPVGPGVGPAGAGSGAGAGS 60
DB 1 GAGAGSGAGAGSGVGPVGVPVGKGVGPVGVPVGPGVGPAGAGSGAGAGS 60
QY 61 GAGAGSGAGAGSGVGPVGVPVGKGVGPVGVPVGPGVGPAGAGSGAGAGS 120
DB 61 GAGAGSGAGAGSGVGPVGVPVGKGVGPVGVPVGPGVGPAGAGSGAGAGS 120

[illegible]

Query Match	100.0%	Score 4173;	DB 16;	Length 780;
Best Local Similarity	100.0%;	Pred. No. 8.9e-248;		
Matches 780; Conservative	0;	Mismatches	0;	Gaps 0;

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Dd	1	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	60
OY	61	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	120
Dd	61	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	120
OY	121	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	180
Dd	121	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	180
OY	181	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	240
Dd	181	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	240
OY	241	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	300
Dd	241	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	300
OY	301	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	360
Dd	301	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	360
OY	361	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	420
Dd	361	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	420
OY	421	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	480
Dd	421	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	480
OY	481	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	540
Dd	481	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	540
OY	541	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	600
Dd	541	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	600
OY	601	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	660
Dd	601	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	660
OY	661	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	720
Dd	661	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	720
OY	721	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	780
Dd	721	GAGAGS	GAGAGSGSVGVPGVGVPBGVPGKGVPGVGPBGVPGVGPBGAGSGAGAGS	780

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RESULT 3
US-10-845-775A-19
/ Sequence 19, Application US/10845775A
/ Publication No. US20040228913A1
/ GENERAL INFORMATION:
/ APPLICANT: Kumar, Manoj
/ APPLICANT: Mazeaud, Isabelle
/ APPLICANT: Cristiano, Steven P.
/ TITLE OF INVENTION: Controlled Release of Active Agents Utilizing Repeat Sequences
/ FILE OF INVENTION: Protein Polymers
/ PILE REFERENCE: DOC 0077 PA/GC 792-6/DC 5110
/ CURRENT APPLICATION NUMBER: US/10/845,775A
/ CURRENT FILING DATE: 2004-05-14
/ PRIOR APPLICATION NUMBER: US 60/470,465
/ PRIOR FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 19
/
/ LENGTH: 780
/ TYPE: PRT
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	Sequence 19, Application US/08806029	
	Publication No. US20020045567A1	
	GENERAL INFORMATION:	
	APPLICANT: Cappello, Joseph	
	APPLICANT: Stedronsky, Erwin R.	
	TITLE OF INVENTION: Synthetic Proteins for in vivo Drug	
	TITLE OF INVENTION: Delivery and Tissue Augmentation	
	NUMBER OF SEQUENCES: 36	
	CORRESPONDENCE ADDRESS:	
	ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert	
	STREET: Four Embarcadero Center, Suite 3400	
	CITY: San Francisco	
	STATE: California	
	COUNTRY: United States	
	ZIP: 94111	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Floppy disk	
	COMPUTER: IBM PC compatible	
	OPERATING SYSTEM: PC-DOS/MS-DOS	
	SOFTWARE: PatentIn Release #1.0, Version #1.30	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/08/806_029	
	FILING DATE: 24-FEB-1997	
	CLASSIFICATION: 514	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US 08/212,237	
	FILING DATE: 11-MAR-1994	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Treccartin, Richard F.	
	REGISTRATION NUMBER: 31,801	
	REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (415) 781-1989	
	TELEFAX: (415) 398-3249	
	INFORMATION FOR SEO ID NO: 19:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 889 amino acids	
	TYPE: amino acid	
	STRANDEDNESS: unknown	
	TOPOLOGY: unknown	
	MOLECULE TYPE: protein	
	US-08-806-029-19	
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Best Local Similarity	92.2%; Pred. No. 3,3e-208;	
Matches 765; Conservative	0; Mismatches 13; Indels 52; Gaps 52;	
OY	3 GAGSAGAGSGVGVPGVGPVGVPBGKVPGVG -PVG- -PVG- -PGAAGSSGGA	58
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Db	94 GSGAGAGSGAGAGSGVGVPGVGPVGVPBGVPGVGPVGVPBGVPAAGS	153
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Db	154 GAGAGSGAGAGSGAGAGSGVGVPGVGPVGVPBGVGPVGVPBGVPAAGS	213
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Db	214 GAGSAGAGSGAGAGSSAGAGSGVGVPGVGPVGVPBGKVPGVG -PVG- -PVG- -PVG	273
OY	228 - PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPBGVPBGKVPVG- -PVG- -PVG-	283
Db	274 VPGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPBGVPBGKVPVGVPVG	333
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OY	341 GVG-PGVG-PGAAGSGAGAGSGAGAGSGAGAGSGVGPVGVPBGVPBGKVPVG- -P	397

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Db      394 GVGVPGVGVPAGAGAGSAGAAGSGAGAGSGAGSVGPVGVPGVPGVPGV 4533
QY      398 VG-PGVG-PCVG-PCAAGASGAAGSAGAAGSGVGVPGVGVPEKKGVPGV 454
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Db      454 VGVPGVGVPGVGVPGAAGSAGAAGSAGAAGSGVGPVGVPGVPGVPGV 5133
QY      455 G-PGVG-PCVG-PCVG-PCAAGASGAAGSAGAAGSGVGVPGVPGVPGK 510
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QY      511 VPVG-VPGV-PCVG-PCVG-PCAAGSAGAAGSAGAAGSGVGVPGVPGV 566
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Db      574 VPGVGVPGVGVPGVGVPGAAGSAGAAGSAGAAGSGVGVPGVPGV 6333
QY      567 PGKGVPGV-PCVG-PCVG-PCVG-PCAAGSAGAAGSAGAAGSGVGVPGV 622
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Db      634 PGVGVPGVGVPGVGVPGAAGSAGAAGSAGAAGSGVGVPGV 6933
QY      623 GVGVPKGVPGV-PCVG-PCVG-PCVG-PCAAGSAGAAGSAGAAGSGVPG 678
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QY      679 VGVPGVPGKGVPGAAGSAGAAGSAGAAGSAGAAGSGV 7344
Db      754 VGVPGVGVPGVGVPGAAGSAGAAGSAGAAGSGVPGV 8133
QY      735 GVPGVPGVPGVPGKGVPGAAGSAGAAGSAGAAGSAGAAGS 780
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Db      814 GVPGVPGVPGVPGVPGVPGAAGSAGAAGSAGAAGSAGAAGS 863

RESULT 6
; 10-117-931-15
; Sequence 15, Application US/10117931
; Publication No. US20030104589A1
GENERAL INFORMATION:
APPLICANT: STEBRONSKY, Erwin R.
CAPPELO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic Crosslinking
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: FLEHR, HOBRACH, TEST, ALBERTSON & HERBERT
STREET: Four Embarcadero Center, Suite 200
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/117,931
FILING DATE: 05-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/642,246
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Berttram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-396-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-117-931-15

Query Match
Best Local Similarity 82.6%; Score 3448; DB 14; Length 884;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

3 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
4 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 93
5 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 114
6 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 153
7 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 170
8 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 213
9 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 227
10 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 273
11 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 283
12 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 333
13 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 340
14 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 393
15 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 397
16 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 453
17 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 454
18 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 513
19 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 510
20 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 573
21 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 566
22 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 633
23 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 622
24 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 693
25 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 678
26 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 753
27 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 734
28 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 813
29 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 780
30 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 863
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TITLE OF INVENTION: Compositions
FILE REFERENCE: DOC 0057 PA / GCT92-4 / DC 5074
CURRENT APPLICATION NUMBER: US/10/800,179
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: 60/454,077
PRIOR FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25
LENGTH: 884
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: SHEL 47E-13
US-10-800-179-25

Query Match
Best Local Similarity 82.6%; Score 3448; DB 16; Length 884;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

3 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
4 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 93
5 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 114
6 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 153
7 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 170
8 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 213
9 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 227
10 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 273
11 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 283
12 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 333
13 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 340
14 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 393
15 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 397
16 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 453
17 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 454
18 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 513
19 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 510
20 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 573
21 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 566
22 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 633
23 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 622
24 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 693
25 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 678
26 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 753
27 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 734
28 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 813
29 GAGSGAGAGSGVGPVGVPVGVPVGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 780
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[illegible]

RESULT 10
US-10-845

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? Sequence 37 Application US/10845936A
? Publication No. US20040234609A1
?
? GENERAL INFORMATION:
? APPLICANT: Collier, Katherine D.
? APPLICANT: Cuevas, William A.
? APPLICANT: Kumar, Manoj A.
? TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
? TITLE OF INVENTION: and Uses
? FILE REFERENCE: D0C0068PA/DCS058/GC792
? CURRENT APPLICATION NUMBER: US/10/845,936A
? CURRENT FILING DATE: 2004-05-14
? PRIOR APPLICATION NUMBER: 60/470,464
? PRIOR FILING DATE: 2003-05-14
? NUMBER OF SEQ ID NOS: 37
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 37
? LENGTH: 983
? TYPE: PRT
? ORGANISM: unknown
? FEATURE:
? OTHER INFORMATION: CBBPhexamer-SELP47K: silk, elastin and cellulose binding peptide
? US-10-845-936A-37

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Query Match	82.6%	Score 3448	DB 17	Length 983
Best Local Similarity	90.6%	Pred. No. 2e-203		
Matches	752	Conservative	0	Matches 26
				Indels 52
				Gaps 52
QY	3	GAGSGAGSGGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA	58	
		GAGSGAGSGGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA	114	
Db	133	GAGSGAGSGGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA	192	
		GAGSGAGSGGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA	248	
QY	59	GSGAGAGSGAGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGAGAGS	114	
		GSGAGAGSGAGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGAGAGS	170	
Db	193	GSGAGAGSGAGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGAGAGS	252	
		GSGAGAGSGAGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGAGAGS	308	
QY	115	GAGAGSGAGAGSGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGA	170	
		GAGAGSGAGAGSGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGA	226	
Db	253	GAGAGSGAGAGSGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGA	312	
		GAGAGSGAGAGSGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGA	368	
QY	171	GAGSGAGAGSGAGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGA	227	
		GAGSGAGAGSGAGAGSGTVPGVGPVGVPKGKVPGVG-PGVG-PGVG-PGVG-PGA	283	

[illegible]

RESULT 11
US-10-845

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: Sequence 32 Application US/10845936A
: Publication No. US20040234609A1
:
: GENERAL INFORMATION:
: APPLICANT: Collier, Katherine D.
: APPLICANT: Cuevas, William A.
: APPLICANT: Kumar, Manoj A.
: TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
: TITLE OF INVENTION: and Uses
: FILE REFERENCE: DOC0068PA/DCS058/GC792
: CURRENT APPLICATION NUMBER: US/10/845, 936A
: CURRENT FILING DATE: 2004-05-14
: PRIOR APPLICATION NUMBER: 60/470,464
: PRIOR FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 32
:
: LENGTH: 1027
: TYPE: PRT
:
: ORGANISM: unknown
: FEATURE:
:
: OTHER INFORMATION: silk and elastin and cecropin A melleitin peptide repeat sequence
: US-10-845-936A-32

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Query Match	82.6%	Score 3448;	DB 17;	Length 1027;
Best Local Similarity	90.6%	Pred. No. 2.1e-203;		
Matches 752; Conservative	0;	Mismatches 26;	Indels 52;	Gaps 52;


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/ Publication No. US20040234609A1
/ GENERAL INFORMATION:
/ APPLICANT: Collier, Katherine D.
/ APPLICANT: Cuevas, William A.
/ APPLICANT: Kumar, Manoj A.
/ TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
/ FILE REFERENCE: DOC00688A/DC5058/GC792
/ CURRENT APPLICATION NUMBER: US/10/845,936A
/ CURRENT FILING DATE: 2004-05-14
/ PRIOR APPLICATION NUMBER: 60/470,464
/ PRIOR FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 34
/ LENGTH: 1125
/ TYPE: PRT
/ ORGANISM: unknown
/ FEATURE:
/ OTHER INFORMATION: GFP-SELP47K: sIk, elastin and green fluorescent protein peptides
US-10-845-936A-34

Query Match      82.6%; Score 3448; DB 17; Length 1125;
Best Local Similarity 90.6%; Pred. No. 2.3e-203;
Matches 752; Conservative 0; Mismatches 26; Indels 52; Gaps 52;

QY 3 GAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 58
DB 275 GAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA 334
QY 59 GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 114
DB 335 GSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGS 394
QY 115 GAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGA 170
DB 395 GAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGA 454
QY 171 GAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGV 227
DB 455 GAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGV 514
QY 228 -GAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG- 283
DB 515 VPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG- 574
QY 284 PGVGV-PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-P 340
DB 575 PGVGV-PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGVG-P 634
QY 341 GVG-PGVG-PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 397
DB 635 GVGPGVGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 694
QY 398 VG-PGVG-PGVG-PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGV 454
DB 695 VGVPGVGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PGK 754
QY 455 G-PGVG-PGVG-PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGK 510
DB 755 GVPGVGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 814
QY 511 VPGVG-PGVG-PGVG-PGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGV 566
DB 815 VPGKGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 874
QY 567 PGKGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 622
DB 875 PGVGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 934
QY 623 GVGPGKGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 678
DB 935 GVGPGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 994
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QY 679 VGVPGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 734
DB 995 VGVPGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 1054
QY 735 GVGPGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 780
DB 1055 GVGPGVPGAAGAGSGAGAGSGAGAGSGVGVPGVGVPGKGVPGVG-PG 1104

RESULT 14
US-10-800-179-31
/ Sequence 31, Application US/10800179
/ Publication No. US20040180027A1
/ GENERAL INFORMATION:
/ APPLICANT: Cuevas, William A.
/ APPLICANT: Kumar, Manoj
/ TITLE OF INVENTION: Use of Repeat Sequence Protein Polymers in Personal Care
/ FILE REFERENCE: DOC 0057 PA / GC792-4 / DC 5074
/ CURRENT APPLICATION NUMBER: US/10/800,179
/ CURRENT FILING DATE: 2004-03-12
/ PRIOR APPLICATION NUMBER: 60/454,077
/ PRIOR FILING DATE: 2003-03-12
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 31
/ LENGTH: 965
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: SELP 58
US-10-800-179-31

Query Match      80.2%; Score 3346; DB 16; Length 965;
Best Local Similarity 82.9%; Pred. No. 3.4e-197;
Matches 744; Conservative 0; Mismatches 33; Indels 120; Gaps 52;

QY 4 AGSGAGAG-SGVGVPGAAGAGSGAGAGSGVGVPGKGVPGVG-PGVG-PGV- 57
DB 29 ASDPMGVPGAAGAGSGAGAGSGVGVPGVPGAAGAGSGAGAGSGAGAGS 88
QY 58 AGSGAGAGSGAGAGSGVGVPGVPGAAGAGSGAGAGSGVGVPGVPGAAGAG 107
DB 89 AGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGAAGAGSGAGAG 148
QY 108 PGAAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGAAGAG 164
DB 149 SGAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGAAGAG 208
QY 165 GV-----GPGAAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSG 216
DB 209 GVGPGAAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGA 268
QY 217 GVG-PGVG-PGV-----GPGAAGAGSGAGAGSGAGAGSGVGVPGAAG 267
DB 269 GVGPGAAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGA 328
QY 268 GKGVPGVG-PGVG-PGV-----GPGAAGAGSGAGAGSGAGAGSGVGVPGA 317
DB 329 GVGPGAAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGA 388
QY 318 GVGPGAAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGA 367
DB 389 GVGPGAAGAGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGA 448
QY 368 AGAGSGVPGAAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGAAG 417
DB 449 AGAGSGVPGAAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGAAG 508
QY 418 AGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGAAGAGSGAGAG 467
DB 509 AGSGAGAGSGAGAGSGVGVPGAAGAGSGAGAGSGVGVPGAAGAGSGAGAG 568
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